

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2004, 03:39:37 ; Search time 4277 Seconds  
(without alignments)  
12595.598 Million cell updates/sec

Title: US-09-668-314C-1  
Perfect score: 1804  
Sequence: 1 atgggcgcactggcccgggc.....aaacaaaaaaaaaaaaaaaaa 1804

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_mam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vrl:\*

28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	%		Query		DB	ID	Description
	No.	Score	Match	Length			
	1	1182.2	65.5	3703	11	AK078770	AK078770 Mus muscu
	2	1177.8	65.3	1810	11	AK052309	AK052309 Mus muscu
	3	1114.4	61.8	1245	29	AY419487	AY419487 Homo sapi
c	4	910	50.4	970	13	BQ688240	BQ688240 AGENCOURT
c	5	894.4	49.6	1015	13	BX401345	BX401345 BX401345
	6	855.8	47.4	1245	29	AY419489	AY419489 Mus muscu
	7	821.6	45.5	1004	13	BX401346	BX401346 BX401346
	8	815.8	45.2	970	29	AY419488	AY419488 Pan trogl
	9	815.2	45.2	908	13	BU179147	BU179147 AGENCOURT
	10	800.6	44.4	912	14	CA489608	CA489608 AGENCOURT
	11	798.8	44.3	968	13	BQ945383	BQ945383 AGENCOURT
	12	792.4	43.9	890	14	CA454208	CA454208 AGENCOURT
	13	785.2	43.5	902	14	CA488936	CA488936 AGENCOURT
	14	777.4	43.1	836	14	CA487940	CA487940 AGENCOURT
	15	777.4	43.1	843	12	BG281374	BG281374 602401870
	16	762.6	42.3	963	13	BQ935923	BQ935923 AGENCOURT
	17	759.8	42.1	925	13	BX390813	BX390813 BX390813
	18	745.4	41.3	1201	13	BX382644	BX382644 BX382644
c	19	741.4	41.1	888	13	BQ690769	BQ690769 AGENCOURT
	20	733.2	40.6	999	14	CA487517	CA487517 AGENCOURT
	21	730.4	40.5	733	12	BG762901	BG762901 602735157
	22	729.4	40.4	846	13	BQ431613	BQ431613 AGENCOURT
	23	727	40.3	887	13	BQ881371	BQ881371 AGENCOURT
	24	725.8	40.2	940	14	CF408400	CF408400 CH3#054_C
c	25	723.4	40.1	730	14	CA448122	CA448122 UI-H-ED1-
	26	717.6	39.8	814	12	BG106472	BG106472 602289863
c	27	717.2	39.8	734	12	BM973950	BM973950 UI-CF-EC1
	28	713	39.5	713	12	BM772694	BM772694 K-EST0056
	29	709.6	39.3	854	12	BG533371	BG533371 601860758
	30	708.4	39.3	934	12	BM013771	BM013771 603639332
	31	706.6	39.2	901	12	BI836576	BI836576 603089550
c	32	705.4	39.1	717	12	BQ000510	BQ000510 UI-H-DP0-
c	33	704	39.0	713	13	BU622591	BU622591 UI-H-FL1-
	34	704	39.0	823	12	BG437126	BG437126 602488768
c	35	699.6	38.8	707	13	BU686888	BU686888 UI-CF-DU1
	36	688.2	38.1	875	12	BG577081	BG577081 602595503
	37	686	38.0	730	10	BE276147	BE276147 601121546
	38	673.4	37.3	700	10	BE276741	BE276741 601144734
	39	670	37.1	931	13	BQ676961	BQ676961 AGENCOURT
	40	666.6	37.0	828	13	BQ721813	BQ721813 AGENCOURT
	41	666	36.9	787	10	BE274684	BE274684 601122323
	42	665.4	36.9	745	12	BG768277	BG768277 602744352
	43	662	36.7	842	12	BG674963	BG674963 602621159
	44	659.2	36.5	1049	12	BM556855	BM556855 AGENCOURT
c	45	658.6	36.5	682	12	BM679834	BM679834 UI-E-EJ0-

## ALIGNMENTS

## RESULT 1

AK078770

LOCUS AK078770 3703 bp mRNA linear HTC 18-SEP-2003

DEFINITION Mus musculus 15 days embryo male testis cDNA, RIKEN full-length enriched library, clone:8030470009 product:beta-site APP-cleaving enzyme 2, full insert sequence.

ACCESSION AK078770

VERSION AK078770.1 GI:26347470

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

## REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

## REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

## REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I &amp; II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

## REFERENCE 6 (bases 1 to 3703)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .3703  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM\_DB:8030470009"  
/db\_xref="MGI:2397197"  
/db\_xref="taxon:10090"  
/clone="8030470009"  
/sex="male"  
/tissue\_type="testis"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="15 days embryo"

CDS 42. .1586  
/note="unnamed protein product; beta-site APP-cleaving enzyme 2 (MGD|MGI:1860440, GB|NM\_019517, evidence: BLASTN, 99%, match=1774)  
putative"  
/codon\_start=1  
/protein\_id="BAC37384.1"  
/db\_xref="GI:26347471"  
/translation="MGALLRALLLPVLAQWLLSAVPALAPAPFTLPLQVARATNHRAS  
AVPGLGTPGLPRADGLALALEPVRATANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKVQ  
ILVDTGSSNFAVAGAPHSYIDTYFDSESSSTYHSKGFDTVVKYTQGSWTGFVGEDLVT  
IPKGFNSSFLVNIATIFESENFFLPGIKWNGILGLAYAALAKPSSSLETFFDLSVAQA  
KIPDIFSMQMCAGLPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILK  
LEIGGQNLNLDCREYNADKAIVDSGTTLLRLPQKVFDVAVVEAVARTSLIPEFSDGFWT  
GAQLACWTNSETPWAYFPKISIIYLRDENASRSFRITILPOLYIQPMMGAGFNIECYRF  
GISSSTNALVIGATVMEGFYVVFDRQRRVGFVSPCAEIEGTTVSEISGPFSTEDIA"



SNCVPAQALNEPILWIVSYALMSVCGAILLVLLLLLLLPLHCRHAPRDPEVVNDESSL  
VRHRWK"

ORIGIN

Query Match 65.5%; Score 1182.2; DB 11; Length 3703;  
Best Local Similarity 80.6%; Pred. No. 1.6e-164;  
Matches 1447; Conservative 0; Mismatches 308; Indels 40; Gaps 4;

```
Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
          ||||| ||| || || || |||| || ||||| ||||| || | ||
Db     42 ATGGGCGCGCTGCTTCGAGCACTCTTGCTCCCGGTGCTGGCGCAGTGGCTCTTGAGTGCG 101

Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
          | ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    102 GTCCCCGCGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCAAGTGGCCCGGGCCACGAAC 161

Qy    121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
          | | || || | || |||| ||||| || | || || |||| | | ||
Db    162 CACAGAGCCTCGGCTGTTCCCGGACTCGGGACCCCGGGTTGCCCGGGCCGATGGTCTG 221

Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
          || |||| | ||||| || | || | ||||| ||||| |||
Db    222 GCCCTCGCACTGGAGCCTGTCAGGGC-----TACTGCCAACTTCTTGGCTATG 269

Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    270 GTGGACAACCTTCAGGGGGACTCTGGCCGCGGCTACTACCTAGAGATGCTGATCGGGACC 329

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
          || ||||| ||||| ||||| || ||||| ||||| || ||||| |||
Db    330 CCTCCGCAGAAGGTACAGATTCTTGTGGACACTGGAAGCAGTAACTTCGCTGTGGCAGGT 389

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
          |||| | ||||| ||||| ||||| ||||| || ||||| ||||| |||||
Db    390 GCCCCACACTCCTACATAGACACCTACTTTGACTCAGAGAGCTCCAGCACATACCACTCC 449

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
          ||||| |||| | ||||| ||||| ||||| ||||| ||||| |||
Db    450 AAGGGCTTTGATGTCACTGTGAAGTACACACAGGGAAGCTGGACTGGCTTTGTTGGTGAG 509

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT 540
          |||| | ||||| ||||| ||||| || |||| | |||| | ||||| |||||
Db    510 GACCTTGTACCATCCCCAAAGGCTTCAACAGCTCTTTCTTGGTCAATATTGCCACTATT 569

Qy    541 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
          || || || ||||| ||||| ||||| ||||| ||||| ||||| || |||
Db    570 TTCGAGTCTGAGAATTTCTTTTGCCTGGTATTAAATGGAATGGAATCCTTGGACTTGCT 629

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
          |||| | | ||||| ||||| ||||| || || || ||||| || |
Db    630 TATGCTGCTTTGGCCAAGCCATCAAGCTCTCTGGAGACATTTTTTGGATTCCCTGGTGGCC 689

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
          ||||| || || || ||||| ||||| ||||| || || || ||||| || |||
Db    690 CAAGCAAAGATTCCAGACATTTTCTCCATGCAGATGTGCGGGGCTGGATTGCCAGTAGCT 749

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
```

Db	750	GGTTCTGGTACCAACGGAGGTAGTCTTGTCTGGGTGGGATTGAACCAAGTTTGTATAAA	809
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	810	GGAGATATCTGGTATAACCCCAATTAAAGAGGAATGGTACTATCAAATAGAAATCCTGAAG	869
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	870	TTGGAAATTGGAGGCCAGAACCTCAACCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	929
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	930	ATTGTGGACAGTGGCACCACGCTCCTGCGCCTGCCCCAGAAGGTGTTTGATGCAGTGGTG	989
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	990	GAAGCTGTGGCACGAACATCTCTGATTCCAGAGTTTTCTGATGGCTTCTGGACAGGGGCC	1049
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1050	CAGCTGGCATGCTGGACAAATTCTGAAACGCCATGGGCATATTTCCCTAAGATTTCTATC	1109
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1110	TACCTGAGAGATGAGAATGCCAGTCGCTCCTTCCGGATCACCATTCTCCACAGCTCTAC	1169
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGGCATTTCCCCA	1200
Db	1170	ATTCAGCCCATGATGGGAGCTGGTTTCAATTATGAATGCTACCGTTTTGGTATCTCCTCT	1229
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1230	TCCACAAATGCGCTGGTGATTGGTGCGACCGTGATGGAAGGCTTCTACGTGGTCTTTGAC	1289
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1290	AGAGCTCAGAGGAGGGTGGGCTTTGCAGTGAGTCCCTGTGCAGAGATTGAAGGTACCACA	1349
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1350	GTGTCTGAAATTTCTGGGCCCTTTTCCACGGAAGACATAGCCAGCAACTGTGTTCAGCA	1409
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1410	CAGGCTCTGAATGAGCCCATCTTGTGGATTGTGTCCTATGCCCTGATGAGTGTGTGTGGA	1469
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1470	GCCATTCTCCTGGTTCTGATCCTCCTCCTGCTGCTCCCGCTGCACTGCCGTCATGCCCCC	1529
Qy	1501	CGTGACCCTGAGGTGCTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1530	CGAGACCCTGAGGTAGTTAACGATGAGTCCTCACTAGTCAGACATCGCTGGAAATGAAGA	1589
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620

Db 1590 GCCTCACCTGAACTCCAGCAGCCTTGAAGCTCAGCTCTTCCAAGAGGGACACCTCCA---- 1645

Qy 1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCCACCCGTCTTCAATCTCTGTTCT 1680  
 | | | | | | | | | | | | | | | | | | | | | |

Db 1646 -----GTTGGCTTCTCTGCCTATTAGTCGGGAACCTCAACTGT 1683

Qy 1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740  
 | | | | | | | | | | | | | | | | | | | | | |

Db 1684 GCAACTGAATGCCTTCCAGACTGTATCT-TGATTACTCTTGATTTCCAAGCTTTCAAGATC 1742

Qy 1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAA 1795  
 | | | | | | | | | | | | | | | | | | | | | |

Db 1743 TTTTCTACTTCAGAGAGAAATGA-TAATAAAAACACCTCATTGTGAACCAAAACA 1796

## RESULT 2

AK052309

LOCUS AK052309 1810 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330025D14 product:beta-site APP-cleaving enzyme 2, full insert sequence.

ACCESSION AK052309

VERSION AK052309.1 GI:26342548

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

## REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

## REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 1810)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .1810  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM\_DB:D330025D14"  
/db\_xref="MGI:2421341"  
/db\_xref="taxon:10090"  
/clone="D330025D14"  
/tissue\_type="heart"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="13 days embryo"

CDS 62. .1606  
/note="unnamed protein product; beta-site APP-cleaving enzyme 2 (MGD|MGI:1860440, GB|NM\_019517, evidence: BLASTN, 99%, match=1774)  
putative"  
/codon\_start=1  
/protein\_id="BAC34931.1"

/db\_xref="GI:26342549"  
/translation="MGALLRALLLPVLAQWLLSAVPALAPAPFTLPLQVARATNHRAS  
AVPGLGTPELPRADGLALALEPVRATANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKVQ  
ILVDTGSSNFAVAGAPHSYIDTYFDSESSSTYHSKGFDVTVKYTQGSWTGFVGEDLVT  
IPKGFNSSFLVNIATIFESENFPLPGIKWNGILGLAYAALAKPSSSLETFDLSVAQA  
KIPDIFSMQMCAGLPVAGSGTNNGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILK  
LEIGGQNLNLDREYNADKAIVDSTLLRLPQKVFDVAVVEAVARTSLIPEFSDGFWT  
GAQLACWTNSETPWAYFPKISYLRDENASRSFRTTILPQLYIQPMMGAGFNYECYRF  
GISSSTNALVIGATVMEGFYVFDRAQRRVGFVAVSPCAEIEGTTVSEISGPFSTEDIA  
SNCVPAQALNEPILWIVSYALMSVCGAILLVLLILLLLPLHCRHAPRDPEVVNDESSL  
VRHRWK"

polyA\_signal 1787. .1792  
/note="putative"  
polyA\_site 1810  
/note="putative"

ORIGIN

Query Match 65.3%; Score 1177.8; DB 11; Length 1810;  
Best Local Similarity 80.5%; Pred. No. 8.7e-164;  
Matches 1431; Conservative 0; Mismatches 307; Indels 39; Gaps 3;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCAGTGGCTCCTGCGCGCC	60
Db	62	ATGGGCGCGCTGCTTCGAGCACTCTTGCTCCCGGTGCTGGCGCAGTGGCTCTTGAGTGCG	121
Qy	61	GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	122	GTCCCCGCGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCAAGTGGCCCGGGCCACGAAC	181
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	182	CACAGAGCCTCGGCTGTTCCCGGACTCGGGACCCCGAGTTGCCCCGGGCGGATGGTCTG	241
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	242	GCCCTCGCACTGGAGCCTGTCAGGGC-----TACTGCCAACTTCTTGGCTATG	289
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	290	GTGGACAACCTTCAGGGGGACTCTGGCCGCGGCTACTACCTAGAGATGCTGATCGGGACC	349
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	350	CCTCCGCAGAAGGTACAGATTCTTGTGGACACTGGAAGCAGTAACTTCGCTGTGGCAGGT	409
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	410	GCCCCACACTCCTACATAGACACCTACTTTGACTCAGAGAGCTCCAGCACATACCACTCC	469
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	470	AAGGGCTTTGATGTCACTGTGAAGTACACACAGGGAAGCTGGACTGGCTTTGTTGGTGAG	529
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	530	GACCTTGTCAACATCCCCAAAGGCTTCAACAGCTCTTTCTTGGTCAATATTGCCACTATT	589

Qy		541	TTTGAATCAGAGAATTCTTTTTGCGCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600	
Db		590	TTCGAGTCTGAGAATTCTTTTTGCGCTGGTATTAAATGGAATGGAATCCTTGGACTIONGCT	649	
Qy		601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660	
Db		650	TATGCTGCTTTGGCCAAGCCATCAAGCTCTCTGGAGACATTTTTTGTATCCCTGGTGACC	709	
Qy		661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCCTTGCT	720	
Db		710	CAAGCAAAGATTCCAGACATTTTCTCCATGCAGATGTGCGGGGCTGGATTGCCAGTAGCT	769	
Qy		721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780	
Db		770	GGTTCTGGTACCAACGGAGGTAGTCTTGTCTTGGGTGGGATTGAACCAAGTTTGTATAAA	829	
Qy		781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840	
Db		830	GGAGATATCTGGTATAACCCCAATTAAAGAGGAATGGTACTATCAAATAGAAATCCTGAAG	889	
Qy		841	TTGGAAATTGGAGGCCAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900	
Db		890	TTGGAAATTGGAGGCCAGAACCCTCAACCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	949	
Qy		901	ATCGTGGACAGTGGCACACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960	
Db		950	ATTGTGGACAGTGGCACACGCTCCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1009	
Qy		961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020	
Db		1010	GAAGCTGTGGCACGAACATCTCTGATTCCAGAGTTTTCTGATGGCTTCTGGACAGGGGCC	1069	
Qy		1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080	
Db		1070	CAGCTGGCATGCTGGACAAATTCTGAAACGCCATGGGCATATTTCCCTAAGATTTCTATC	1129	
Qy		1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140	
Db		1130	TACCTGAGAGATGAGAATGCCAGTCGCTCCTTCCGGACCACCATTTCTCCACAGCTCTAC	1189	
Qy		1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200	
Db		1190	ATTCAGCCCATGATGGGAGCTGGTTTCAATTATGAATGCTACCGTTTTGGTATCTCCTCT	1249	
Qy		1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260	
Db		1250	TCCACAAATGCGCTGGTGATTGGTGCGACCGTGATGGAAGGCTTCTACGTGGTCTTTGAC	1309	
Qy		1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320	
Db		1310	AGAGCTCAGAGGAGGGTGGGCTTTGCAGTGAGTCCTGTGCAGAGATTGAAGGTACCACA	1369	
Qy		1321	GTGTCTGAAATTTCCGGGCCCTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380	
Db		1370	GTGTCTGAAATTTCTGGGCCCTTTTCCACGGAAGACATAGCCAGCAACTGTGTCCAGCA	1429	
Qy		1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440	



```

      ||| || ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1430 CAGGCTCTGAATGAGCCCATCTTGTGGATTGTGTCCTATGCCCTGATGAGTGTGTGTGGA 1489

Qy      1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC 1500
      ||||| ||||| || | ||| ||||| ||||| ||| | | || | |||
Db      1490 GCCATTCTCCTGGTTCTGATCCTCCTCCTGCTGCTCCCCTGCACTGCCGTCATGCCCCC 1549

Qy      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
      || ||||| ||||| || || ||||| ||||| || ||||| ||||| |||||
Db      1550 CGAGACCCTGAGGTAGTTAACGATGAGTCCTCACTAGTCAGACATCGCTGGAAATGAAGA 1609

Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
      ||| ||||| ||| |||| || ||||| ||||| || | | ||| ||||
Db      1610 GCCTCACCTGAACTCCAGCAGCCTTGAACCTCAGCTCTTCCAAGAGGGACACCTCCA---- 1665

Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
      | | || || |||| | ||| || ||| | |
Db      1666 -----GTTGGCTTCTCTGCCTATTAGTCGGGAACCTCAACTGT 1703

Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
      || | ||||| ||| | | | | ||||| ||||| ||||| |||
Db      1704 GCAACTGAATGCCTTCCAGACTGTATCT-TGATTACTCTTGATTTCCAAGCTTTCAGATC 1762

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCT 1777
      | ||||| ||| |||| || | |||| | ||
Db      1763 TTTTCTACTTCAGAGAGAAATGATAATAAAAACACCT 1799

```

# RESULT 3

AY419487

LOCUS AY419487 1245 bp DNA linear GSS 17-DEC-2003

DEFINITION Homo sapiens BACE2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY419487

VERSION AY419487.1 GI:39775444

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1245)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1245)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA



COMMENT        These sequences were made by sequencing genomic exons and ordering them based on alignment.

FEATURES                    Location/Qualifiers  
    source                    1. .1245  
                              /organism="Homo sapiens"  
                              /mol\_type="genomic DNA"  
                              /db\_xref="taxon:9606"  
    gene                      <1. .>1245  
                              /gene="BACE2"  
                              /locus\_tag="HCM6907"

ORIGIN

Query Match                    61.8%;    Score 1114.4;    DB 29;    Length 1245;  
Best Local Similarity        89.6%;    Pred. No. 2.1e-154;  
Matches 1115;    Conservative        0;    Mismatches    130;    Indels        0;    Gaps        0;

Qy	313	CTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCC	372
Db	1	CTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCC	60
Qy	373	TACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGGGCTTTGAC	432
Db	61	TACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGGGCTTTGAC	120
Qy	433	GTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACC	492
Db	121	GTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACC	180
Qy	493	ATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTGAATCAGAG	552
Db	181	ATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTGAATCAGAG	240
Qy	553	AATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTATGCCCACTT	612
Db	241	AATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTATGCCCACTT	300
Qy	613	GCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAAGCAAACATC	672
Db	301	GCCAAGNN	360
Qy	673	CCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACC	732
Db	361	NN	420
Qy	733	AACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGG	792
Db	421	NNNNNNNNNNNNNNNGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGG	480
Qy	793	TATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGA	852
Db	481	TATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGA	540
Qy	853	GGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGT	912
Db	541	GGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGT	600
Qy	913	GGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAAGCTGTGGCC	972

```

      |||
Db      601 GGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGGAAGCTGTGGCC 660

Qy      973 CGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGC 1032
      |||
Db      661 CGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGC 720

Qy     1033 TGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGAT 1092
      |||
Db      721 TGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGAC 780

Qy     1093 GAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATG 1152
      |||
Db      781 GAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATG 840

Qy     1153 ATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCATCCACAAATGCG 1212
      |||
Db      841 ATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCATCCACAAATGCG 900

Qy     1213 CTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAG 1272
      |||
Db      901 CTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAG 960

Qy     1273 AGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATT 1332
      |||
Db      961 AGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATT 1020

Qy     1333 TCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGC 1392
      |||
Db     1021 TCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGC 1080

Qy     1393 GAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTT 1452
      |||
Db     1081 GAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTT 1140

Qy     1453 GTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAG 1512
      |||
Db     1141 GTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAG 1200

Qy     1513 GTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGA 1557
      |||
Db     1201 GTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGA 1245

```

#### RESULT 4

BQ688240/c

```

LOCUS      BQ688240                      970 bp    mRNA    linear    EST 15-JUL-2002
DEFINITION AGENCOURT_8034236 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6208269
           5', mRNA sequence.
ACCESSION  BQ688240
VERSION    BQ688240.1  GI:21813556
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 970)

```

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCM2365 row: k column: 22  
 High quality sequence stop: 631.

FEATURES Location/Qualifiers  
 source 1. .970  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6208269"  
 /tissue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI;  
 Site\_2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

#### ORIGIN

Query Match 50.4%; Score 910; DB 13; Length 970;  
 Best Local Similarity 98.3%; Pred. No. 2.5e-124;  
 Matches 930; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

Qy	829	GAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAAC	888
Db	954	GAAATTCTGAAATTGGAATTTGGAGCCCAAGCCTTAATCTGGACTGCAGAGAGTATAAC	895
Qy	889	GCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTT	948
Db	894	GCAGCCAAGGCCATCGTGACCAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTT	835
Qy	949	GATGCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTC	1008
Db	834	GATGCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTC	775
Qy	1009	TGGACTGGGTCCC-AGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCC	1067
Db	774	TGGACTGGGTCCCAAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCC	715
Qy	1068	TAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCT	1127
Db	714	TAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCT	655

Qy 1128 GCCTCAGCTTTACATTCAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACCGATT 1187  
 |||  
 Db 654 GCCTCAGCTTTACATTCAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACCGATT 595

Qy 1188 CGGCATTTCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTA 1247  
 |||  
 Db 594 CGGCATTTCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTA 535

Qy 1248 CGTCATCTTCGACAGAGCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAAT 1307  
 |||  
 Db 534 CGTCATCTTCGACAGAGCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAAT 475

Qy 1308 TGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAA 1367  
 |||  
 Db 474 TGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAA 415

Qy 1368 CTGTGTCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCAT 1427  
 |||  
 Db 414 CTGTGTCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCAT 355

Qy 1428 GAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTG 1487  
 |||  
 Db 354 GAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTG 295

Qy 1488 TCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCG 1547  
 |||  
 Db 294 TCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCG 235

Qy 1548 CTGGAAATGAATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATC 1607  
 |||  
 Db 234 CTGGAAATGAATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATC 175

Qy 1608 ACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTT 1667  
 |||  
 Db 174 ACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTT 115

Qy 1668 CAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTC 1727  
 |||  
 Db 114 CAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTC 55

Qy 1728 AAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAAAAAAA 1773  
 |||  
 Db 54 AAGCTTTCAAATCCTCCCTACTTCCAAGAAAAAAA 9

# RESULT 5

BX401345/c

LOCUS BX401345 1015 bp mRNA linear EST 13-MAY-2003

DEFINITION BX401345 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens  
 cDNA clone CS0DK012YC20 3-PRIME, mRNA sequence.

ACCESSION BX401345

VERSION BX401345.1 GI:30614534

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1015)  
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 10331.f For  
 more information about this cluster, see  
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DK012BB10NP1&cluster=10331.f)  
[cgi-bin/cluster.cgi?seq=CS0DK012BB10NP1&cluster=10331.f](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DK012BB10NP1&cluster=10331.f). Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DK012BB10NP1.

FEATURES Location/Qualifiers  
 source 1. .1015  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DK012YC20"  
 /cell\_type="HELA CELLS COT 25-NORMALIZED"  
 /cell\_line="HELA"  
 /clone\_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

# ORIGIN

Query Match 49.6%; Score 894.4; DB 13; Length 1015;  
 Best Local Similarity 97.5%; Pred. No. 4.9e-122;  
 Matches 948; Conservative 12; Mismatches 6; Indels 6; Gaps 5;

Qy	827	TAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATA	886
Db	1015	TAGAAATTCTGAAA-TGGAAATTGGAGGCCMAAAGCCTTAATCTGGACTGCAGAGAGTATA	957
Qy	887	ACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGT	946
Db	956	ACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTS--GCGCCTGCCCCAGAAGGTGT	899
Qy	947	TTGATGCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTT	1006
Db	898	TTGATGCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTT	839
Qy	1007	TCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCC	1066
Db	838	TCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCC	779
Qy	1067	CTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCC	1126
Db	778	CTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCC	719
Qy	1127	TGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGAT	1186

Db 718 TGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGAT 659

Qy 1187 TCGGCATTTCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCT 1246  
 |||

Db 658 TCGGCATTTCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCT 599

Qy 1247 ACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAA 1306  
 |||

Db 598 ACGTCATCTTCGACAGAGCCCAGAAGAGGGT-GGSTTCGCAGCGAGCCCCTGTGCAGAAA 540

Qy 1307 TTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCA 1366  
 |||

Db 539 TTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCA 480

Qy 1367 ACTGTGTCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCA 1426  
 |||

Db 479 ACTGTGTCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCA 420

Qy 1427 TGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGT 1486  
 |||

Db 419 TGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTG-CGTTCCGGT 361

Qy 1487 GTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATC 1546  
 |||

Db 360 GTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATC 301

Qy 1547 GCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAAT 1606  
 |||

Db 300 GCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAAT 241

Qy 1607 CACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCT 1666  
 |||

Db 240 CACATTTCCAGGGCAGCAGCMGGGATCGAHGGTGGCGCTHTCTCCTGTGCCACCCSTCH 181

Qy 1667 TCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTT 1726  
 |||

Db 180 TCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATACACTGTCTTTTGATTCTTGATTTT 121

Qy 1727 CAA-GCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTA 1785  
 |||

Db 120 CAAGGCTTTCAAATCCTCCCGRCTTCCAAGAMAAATAATTAAAAAAAACCTTCATTCTA 61

Qy 1786 AACCAAAAAAAA 1797  
 | : |||| | |

Db 60 ATYCAAACAGA 49

# RESULT 6

AY419489

LOCUS AY419489 1245 bp DNA linear GSS 17-DEC-2003

DEFINITION Mus musculus BACE2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY419489

VERSION AY419489.1 GI:39775446

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1245)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1245)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT These sequences were made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES Location/Qualifiers

source 1. .1245  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"

gene <1. .>1245  
/gene="BACE2"  
/locus\_tag="HCM6907"

# ORIGIN

Query Match 47.4%; Score 855.8; DB 29; Length 1245;  
Best Local Similarity 76.6%; Pred. No. 2.2e-116;  
Matches 953; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

Qy 314 TACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCCT 373  
||||||| || ||||||||||||||||| || ||||||| ||| |||||

Db 2 TACAGATTCTTGTGGACACTGGAAGCAGTAACTTCGCTGTGGCAGGTGCCCCACACTCCT 61

Qy 374 ACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGGGCTTTGACG 433  
||||||| ||||||| ||||| || ||||||||| ||||||||| |||

Db 62 ACATAGACACCTACTTTGACTCAGAGAGCTCCAGCACATACCACTCCAAGGGCTTTGATG 121

Qy 434 TCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCA 493  
||| ||||||||||||| ||||||||| |||| |||| || ||||| |||||

Db 122 TCACTGTGAAGTACACACAGGGAAGCTGGACTGGCTTTGTTGGTGAGGACCTTGTCACCA 181

Qy 494 TCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATTTTGAATCAGAGA 553  
||| ||||||||| | |||| | |||| ||||||||| || || |||

Db 182 TCCCCAAAGGCTTCAACAGCTCTTCTTGGTCAATATTGCCACTATTTTCGAGTCTGAGA 241

Qy 554 ATTTCTTTTTCGCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTATGCCACACTTG 613  
||||||||||| ||||||||| |||| || ||||||| | |

Db 242 ATTTCTTTTTCGCTGGTATTAAATGGAATGGAATCCTTGGACTTGCTTATGCTGCTTTGG 301

Qy 614 CCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAAGCAAACATCC 673  
|||||



[illegible]



Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	240	GCCCCGGAGCTGGCMCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	299
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	300	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	359
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	360	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	419
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	420	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	479
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	480	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	539
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	540	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	599
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	600	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	659
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	660	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	719
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	720	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	779
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	780	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	839
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	840	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	899
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	900	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	959
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTAC	822
Db	960	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTAC	1001

RESULT 8

AY419488

LOCUS AY419488

970 bp

DNA

linear

GSS 17-DEC-2003

DEFINITION Pan troglodytes BACE2 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION AY419488

VERSION AY419488.1 GI:39775445

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 970)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 970)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT These sequences were made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .970

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

gene <1. .>970

/gene="BACE2"

/locus\_tag="HCM6907"

ORIGIN

Query Match 45.2%; Score 815.8; DB 29; Length 970;

Best Local Similarity 84.5%; Pred. No. 1.8e-110;

Matches 820; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

Qy 334 GGAAGCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGAC 393

|||||

Db 1 GGAAGCAGTAACTTTGNNNTGGCAGGAACCCCGCNNNNNNNNNATAGACACGTACTTNNNC 60

Qy 394 ACAGAGAGGTCTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAA 453

|||||

Db 61 ACAGAGAGGTCTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAA 120

Qy 454 GGAAGCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACT 513

|||||

Db 121 GGAAGCTGGACGGGTTTCGTTGGGGAAGACTTCGTCACCATCCCCAAAGGCTTCAATACT 180

Qy 514 TCTTTTCTTGTCAACATTGCCACTATTTTGAATCAGAGAATTTCTTTTGCCTGGGATT 573

|||||

Db 181 TCTTTTCTTGTCAACATTGCCACTATTTTGAATCAGAGAATTTCTTTTGCCTGGGATT 240

Qy	574	AAATGGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTG	633
Db	241	AAATGGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGNNNNNNNNNNNNNNNN	300
Qy	634	GAGACCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAG	693
Db	301	NN	360
Qy	694	ATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTG	753
Db	361	NNNGTCTTG	420
Qy	754	GGTGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAG	813
Db	421	GGTGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAG	480
Qy	814	TGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGAC	873
Db	481	TGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGAC	540
Qy	874	TGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTG	933
Db	541	TGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGTCTG	600
Qy	934	CCCCAGAAGGTGTTTGATGCGGTGGTGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAA	993
Db	601	CCCCAGAAGGTGTTTGATGCGGTGGTGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAA	660
Qy	994	TTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCT	1053
Db	661	TTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCT	720
Qy	1054	TGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTC	1113
Db	721	TGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCATTC	780
Qy	1114	CGTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTAT	1173
Db	781	CGTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTGAATTAT	840
Qy	1174	GAATGTTACCGATTTCGGCATTTCCTCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTG	1233
Db	841	GAATGTTACCGATTTCGGCATTTCCTCCATCCACAAACGCGCTGGTGATCGGTGCCACGGTG	900
Qy	1234	ATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGC	1293
Db	901	ATGGAGGGCTTCTATGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGC	960
Qy	1294	CCCTGTGCAG	1303
Db	961	CCCTGTGCAG	970

RESULT 9

BU179147

LOCUS BU179147 908 bp mRNA linear EST 04-SEP-2002  
 DEFINITION AGENCOURT\_8050401 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6089176

5', mRNA sequence.

ACCESSION BU179147

VERSION BU179147.1 GI:22693131

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 908)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM2328 row: i column: 17  
High quality sequence stop: 673.

FEATURES Location/Qualifiers

source 1. .908  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6089176"  
/tissue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_112"  
/note="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCACGAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

#### ORIGIN

Query Match 45.2%; Score 815.2; DB 13; Length 908;  
Best Local Similarity 97.9%; Pred. No. 2.3e-110;  
Matches 879; Conservative 0; Mismatches 13; Indels 6; Gaps 5;

Qy	424	GGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGAC	483
Db	1	GGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGAC	60
Qy	484	CTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATTTTT	543
Db	61	CTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATTTTT	120
Qy	544	GAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTAT	603
Db	121	GAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTAT	180



Qy	604	GCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAA	663
Db	181	GCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAA	240
Qy	664	GCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGA	723
Db	241	GCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGA	300
Qy	724	TCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGA	783
Db	301	TCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGA	360
Qy	784	GACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTG	843
Db	361	GACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTG	420
Qy	844	GAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATC	903
Db	421	GAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATC	480
Qy	904	GTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAA	963
Db	481	GTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAA	540
Qy	964	GCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG	1023
Db	541	GCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG	600
Qy	1024	CTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTAC	1083
Db	601	CTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTAC	660
Qy	1084	CTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATT	1143
Db	661	CTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATT	720
Qy	1144	CAGCCCATGATGGGGGCCGG-CCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCATC	1202
Db	721	CAGCCCATGATGGGGGCCGGCCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCATC	780
Qy	1203	CACAAATGC-GCTGGTGATCGGTGCCACGGT--GATGGAGGGCTTCTACGTCATCTTCCA	1259
Db	781	CACAAATGCGGCTGGTGATCGGTGCCACGGTTGATGGAGGGCCTTCTACGTCATCTTCCA	840
Qy	1260	CAGAGCCCAGAAGAGGGT-GGGCTTCGCAGCGAG-CCCCTGTGCAGAAATTGCAGGTG	1315
Db	841	CAGACCCCAAAGAGGGTGGGGTTTCCCAGCGAGCCCCCTGTGCAAAAATTGCAGGGG	898

RESULT 10

CA489608

LOCUS CA489608 912 bp mRNA linear EST 14-NOV-2002

DEFINITION AGENCOURT\_10810689 MAPcL Homo sapiens cDNA clone IMAGE:6722086 5', mRNA sequence.

ACCESSION CA489608

VERSION CA489608.1 GI:24952399



KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 912)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Kristi A. Egland, Ira Pastan  
 cDNA Library Preparation: Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM14284 row: d column: 22  
 High quality sequence stop: 663.  
 FEATURES Location/Qualifiers  
 source 1. .912  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6722086"  
 /cell\_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,  
 hTERT-HME1, LNCaP"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MAPcL"  
 /note="Vector: pCMV-SPORT6; Site\_1: EcoRV; Site\_2: Not I;  
 Subtracted with brain, liver, lung, kidney and muscle.  
 Directionally cloned. Priming method: oligo-dT. Average  
 insert size: 1800 bp. Library amplification: 26,000 fold.  
 Kristi A. Egland, James J. Vincent, Robert Strausberg,  
 Bungkook Lee & Ira Pastan: Discovery of new breast  
 cancer genes encoding membrane and secreted proteins.  
 Manuscript submitted."  
 ORIGIN  
 Query Match 44.4%; Score 800.6; DB 14; Length 912;  
 Best Local Similarity 97.5%; Pred. No. 3.2e-108;  
 Matches 857; Conservative 0; Mismatches 14; Indels 8; Gaps 4;  
 Qy 440 TGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCA 499  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 TGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCA 60  
 Qy 500 AAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTGAATCAGAGAATTTCT 559  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 AAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTGAATCAGAGAATTTCT 120  
 Qy 560 TTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGC 619  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 TTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGC 180  
 Qy 620 CATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAACG 679

```

      |||
Db      181 CATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAACG 240
Qy      680 TTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAG 739
      |||
Db      241 TTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAG 300
Qy      740 GTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCC 799
      |||
Db      301 GTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCC 360
Qy      800 CTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAA 859
      |||
Db      361 CTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAA 420
Qy      860 GCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCA 919
      |||
Db      421 GCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCA 480
Qy      920 CGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAAGCTGTGGCCCGCGCAT 979
      |||
Db      481 CGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAAGCTGTGGCCCGCGCAT 540
Qy      980 CTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGA 1039
      |||
Db      541 CTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGA 600
Qy      1040 ATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACT 1099
      |||
Db      601 ATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACT 660
Qy      1100 CCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTAGCCCATGATGGGGG 1159
      |||
Db      661 CCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTAGCCCATGATGGGGG 720
Qy      1160 CCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCATCCAC-AAATGCGCTGGTG 1218
      |||
Db      721 CCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCATCCACAAAATGCGCTGGTG 780
Qy      1219 ATCGGTGC---CACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGA---AG 1272
      |||
Db      781 ATCGGTGCCCACGGTGAATGGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAAAGAA 840
Qy      1273 AGGGTGGGCTTCGCAGCG-AGCCCCTGTGCAGAAATTGC 1310
      ||
Db      841 GGGTGGGCTTCGCAGCGAACCCCTGTGCAGAAATTGC 879

```

RESULT 11

BQ945383

LOCUS BQ945383 968 bp mRNA linear EST 21-AUG-2002  
 DEFINITION AGENCOURT\_10030827 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6481468  
 5', mRNA sequence.  
 ACCESSION BQ945383  
 VERSION BQ945383.1 GI:22360861  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)



Qy	292	ATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCC	351
Db	241	ATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCC	300
Qy	352	GTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACA	411
Db	301	GTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACA	360
Qy	412	TACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTC	471
Db	361	TACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTC	420
Qy	472	GTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATT	531
Db	421	GTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATT	480
Qy	532	GCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTT	591
Db	481	GCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTT	540
Qy	592	GGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC	651
Db	541	GGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC	600
Qy	652	CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTG	711
Db	601	CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTG	660
Qy	712	CCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGT	771
Db	661	CCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGT	720
Qy	772	TTGTATAAAGGAGACATCTGGTATA-CCCCTATTAAGGAAGAGTGGTACTACCAGATAGA	830
Db	721	TTGTATAAAGGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGA	780
Qy	831	AATTCTGAAATTGGAAATT-GGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAA-C	888
Db	781	AATTCTGGAATTGGAAATTGGGAGCCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACC	840
Qy	889	GCAGACAAGGCCATCGTGGACAGTGGCACCACGC	922
Db	841	GCAGACAAGGCCATCGTGGACAGTGGCACCACGC	874

# RESULT 12

CA454208

LOCUS CA454208 890 bp mRNA linear EST 12-NOV-2002

DEFINITION AGENCOURT\_10738679 MAPcL Homo sapiens cDNA clone IMAGE:6718872 5', mRNA sequence.

ACCESSION CA454208

VERSION CA454208.1 GI:24903721

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 890)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Kristi A. Egland, Ira Pastan  
cDNA Library Preparation: Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM14275 row: n column: 24  
High quality sequence stop: 651.

FEATURES Location/Qualifiers

source 1. .890  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6718872"  
/cell\_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1, LNCaP"  
/lab\_host="EMDH10B"  
/clone\_lib="MAPcL"  
/note="Vector: pCMV-SPORT6; Site\_1: EcoRV; Site\_2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."

#### ORIGIN

Query Match 43.9%; Score 792.4; DB 14; Length 890;  
Best Local Similarity 97.9%; Pred. No. 5.1e-107;  
Matches 856; Conservative 0; Mismatches 11; Indels 7; Gaps 5;

Qy	704	CCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTG	763
Db	1	CCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTG	60
Qy	764	AACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACC	823
Db	61	AACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACC	120
Qy	824	AGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGT	883
Db	121	AGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGT	180
Qy	884	ATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGG	943
Db	181	ATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGG	240
Qy	944	TGTTTGATGCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATG	1003

```

      |||
Db      241 TGTTTGATGCGGTGGTGGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATG 300

Qy      1004 GTTTCCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACT 1063
      |||
Db      301 GTTTCCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACT 360

Qy      1064 TCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAA 1123
      |||
Db      361 TCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAA 420

Qy      1124 TCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACC 1183
      |||
Db      421 TCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACC 480

Qy      1184 GATTCGGCATTTCCTCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCT 1243
      |||
Db      481 GATTCGGCATTTCCTCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCT 540

Qy      1244 TCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAG 1303
      |||
Db      541 TCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAG 600

Qy      1304 AAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCA 1363
      |||
Db      601 AAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCA 660

Qy      1364 GCAACTGTGTCCCGCTCAGTCTTTGAGCGAGCCCA-TTTTGTGGATTGTGTCCTATGCG 1422
      |||
Db      661 GCAACTGTGTCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCG 720

Qy      1423 CTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTT- 1481
      |||
Db      721 CTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCCTTC 780

Qy      1482 CCGGTGTCAGCGTCGCCCCC--GTGACCCTGAGGTCGTCAATGATG-AGTCCTCTCTGGT 1538
      |||
Db      781 CCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAAGTCCTCTCTGGT 840

Qy      1539 CAGACAT--CGCTGGAAATGAATAGCCAGGCCTG 1570
      |||
Db      841 CAGACATTCGCTGGAAAATTAATAGCCAGGCCTG 874

```

# RESULT 13

CA488936

LOCUS CA488936 902 bp mRNA linear EST 14-NOV-2002

DEFINITION AGENCOURT\_10808280 MAPcL Homo sapiens cDNA clone IMAGE:6721142 5', mRNA sequence.

ACCESSION CA488936

VERSION CA488936.1 GI:24951727

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 902)



AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Kristi A. Egland, Ira Pastan  
 cDNA Library Preparation: Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM14281 row: m column: 14  
 High quality sequence stop: 596.

FEATURES Location/Qualifiers  
 source 1. .902  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6721142"  
 /cell\_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,  
 hTERT-HME1, LNCaP"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MAPcL"  
 /note="Vector: pCMV-SPORT6; Site\_1: EcoRV; Site\_2: Not I;  
 Subtracted with brain, liver, lung, kidney and muscle.  
 Directionally cloned. Priming method: oligo-dT. Average  
 insert size: 1800 bp. Library amplification: 26,000 fold.  
 Kristi A. Egland, James J. Vincent, Robert Strausberg,  
 Bungkook Lee & Ira Pastan: Discovery of new breast  
 cancer genes encoding membrane and secreted proteins.  
 Manuscript submitted."

#### ORIGIN

Query Match 43.5%; Score 785.2; DB 14; Length 902;  
 Best Local Similarity 98.9%; Pred. No. 5.8e-106;  
 Matches 801; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy	680	TTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAG	739
Db	1	TTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAG	60
Qy	740	GTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCC	799
Db	61	GTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCC	120
Qy	800	CTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAA	859
Db	121	CTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAA	180
Qy	860	GCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCA	919
Db	181	GCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCA	240
Qy	920	CGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAAGCTGTGGCCCGCGCAT	979
Db	241	CGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAAGCTGTGGCCCGCGCAT	300



Qy 980 CTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGA 1039  
 |||  
 Db 301 CTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGA 360

Qy 1040 ATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACT 1099  
 |||  
 Db 361 ATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACT 420

Qy 1100 CCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTAGCCCATGATGGGGG 1159  
 |||  
 Db 421 CCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTAGCCCATGATGGGGG 480

Qy 1160 CCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCATCCACAAATGCGCTGGTGA 1219  
 |||  
 Db 481 CCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCATCCACAAATGCGCTGGTGA 540

Qy 1220 TCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGG 1279  
 |||  
 Db 541 TCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGG 600

Qy 1280 GCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGC 1339  
 |||  
 Db 601 GCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGC 660

Qy 1340 CTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCTCAGTCTTTGAGCGAGCCCA 1399  
 |||  
 Db 661 CTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCTCAGTCTTTGAGCGAGCCCA 720

Qy 1400 -TTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTA 1458  
 |||  
 Db 721 TTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTA 780

Qy 1459 ATCGTCCTGCTGCTGCTGCCGTTCCGGTGT 1488  
 |||  
 Db 781 ATCGTCCTGCTGCTGCTGCCGTTCCGGTGT 810

# RESULT 14

CA487940

LOCUS CA487940 836 bp mRNA linear EST 14-NOV-2002

DEFINITION AGENCOURT\_10810992 MAPcL Homo sapiens cDNA clone IMAGE:6719667 5', mRNA sequence.

ACCESSION CA487940

VERSION CA487940.1 GI:24948478

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 836)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Kristi A. Egland, Ira Pastan

cDNA Library Preparation: Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM14277 row: p column: 03  
 High quality sequence stop: 629.

FEATURES	Location/Qualifiers
source	1. .836 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6719667" /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1, LNCaP" /lab_host="EMDH10B" /clone_lib="MAPcL" /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."

#### ORIGIN

Query Match 43.1%; Score 777.4; DB 14; Length 836;  
 Best Local Similarity 98.2%; Pred. No. 8.4e-105;  
 Matches 818; Conservative 0; Mismatches 11; Indels 4; Gaps 3;

Qy	468	CTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC	527
Db	1	CTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC	60
Qy	528	CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAAT	587
Db	61	CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAAT	120
Qy	588	ACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGA	647
Db	121	ACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGA	180
Qy	648	CTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGG	707
Db	181	CTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGG	240
Qy	708	CTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACC	767
Db	241	CTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACC	300
Qy	768	AAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGAT	827
Db	301	AAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGAT	360
Qy	828	AGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAA	887

```

|||||
Db      361 AGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAA 420

Qy      888 CGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTT 947
|||||

Db      421 CGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTT 480

Qy      948 TGATGCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTT 1007
|||||

Db      481 TGATGCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTT 540

Qy      1008 CTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCC 1067
|||||

Db      541 CTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCC 600

Qy      1068 TAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCT 1127
|||||

Db      601 TAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCT 660

Qy      1128 GCCTCAGCTTTACATTCAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTA-CCGAT 1186
|||||

Db      661 GCCTCAGCTTTACATTCAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACCCGAT 720

Qy      1187 TCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCA-CGGTGATGGAGGGCTTC 1245
|||||

Db      721 TCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACCGTTGATGGAGGGCTTC 780

Qy      1246 TACGTCATCTTCGACAGAGCCCGAGAA--GAGGGTGGGCTTCGACGAGCCCC 1296
|||||

Db      781 TACGTCATCTTCGACAGAGCCCCGAAAGAGGGTGGGGCTTCGCAACGAGCCCC 833

```

# RESULT 15

BG281374

LOCUS BG281374 843 bp mRNA linear EST 21-FEB-2001

DEFINITION 602401870F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:4544392 5', mRNA sequence.

ACCESSION BG281374

VERSION BG281374.1 GI:13030299

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 843)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)

Plate: LLCM1227 row: k column: 17

```

FEATURES
    source
        Location/Qualifiers
            1. .843
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:4544392"
            /tissue_type="melanotic melanoma"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_20"
            /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
            EcoRI; cDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5'
            adaptor: GGCACGAG(G). Size-selected >500bp for average
            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match 43.1%; Score 777.4; DB 12; Length 843;  
Best Local Similarity 97.7%; Pred. No. 8.3e-105;  
Matches 820; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

<b>Qy</b>	<b>765</b>	<b>ACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCA</b>	<b>824</b>
<b>Db</b>	<b>6</b>	<b>AACCAAGTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCA</b>	<b>65</b>
<b>Qy</b>	<b>825</b>	<b>GATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTA</b>	<b>884</b>
<b>Db</b>	<b>66</b>	<b>GATAGAAATTCTGAAATTGGAAA-TGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTA</b>	<b>124</b>
<b>Qy</b>	<b>885</b>	<b>TAACGCAGACAAGGCCATCGTGGACAGTGGCACACGCTGCTGCGCCTGCCCCAGAAGGT</b>	<b>944</b>
<b>Db</b>	<b>125</b>	<b>TAACGCAGACAAGGCCATCGTGGACAGTGGCACACGCTGCTGCGCCTGCCCCAGAAGGT</b>	<b>184</b>
<b>Qy</b>	<b>945</b>	<b>GTTTGATGCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGG</b>	<b>1004</b>
<b>Db</b>	<b>185</b>	<b>GTTTGATGCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGG</b>	<b>244</b>
<b>Qy</b>	<b>1005</b>	<b>TTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTT</b>	<b>1064</b>
<b>Db</b>	<b>245</b>	<b>TTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTT</b>	<b>304</b>
<b>Qy</b>	<b>1065</b>	<b>CCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAAT</b>	<b>1124</b>
<b>Db</b>	<b>305</b>	<b>CCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAAT</b>	<b>364</b>
<b>Qy</b>	<b>1125</b>	<b>CCTGCCTCAGCTTTACATT CAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCG</b>	<b>1184</b>
<b>Db</b>	<b>365</b>	<b>CCTGCCTCAGCTTTACATT CAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCG</b>	<b>424</b>
<b>Qy</b>	<b>1185</b>	<b>ATTCGGCATT TCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTT</b>	<b>1244</b>
<b>Db</b>	<b>425</b>	<b>ATTCGGCATT TCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTT</b>	<b>484</b>
<b>Qy</b>	<b>1245</b>	<b>CTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGA</b>	<b>1304</b>

Db	485	CTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGA	544
Qy	1305	AATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAG	1364
Db	545	AATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAG	604
Qy	1365	CAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCT	1424
Db	605	CAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCT	664
Qy	1425	CATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCG	1484
Db	665	CATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCG	724
Qy	1485	GTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACA	1544
Db	725	GTGTCAGCGTCGCCCCCGTGA-CCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACA	783
Qy	1545	TCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAA	1603
Db	784	TCGTGGAAAATGAATAGCCAGG-CTGAACTCAAGCAAACATGAACTCAGTATTAGAAAA	841

Search completed: February 28, 2004, 07:03:45  
Job time : 4288 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2004, 02:43:37 ; Search time 6893 Seconds  
(without alignments)  
11343.513 Million cell updates/sec

Title: US-09-668-314C-1  
Perfect score: 1804  
Sequence: 1 atgggcgcactggcccgggc.....aaaccaaaaaaaaaaaaaaa 1804

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*



28: em\_un:\*  
 29: em\_vi:\*  
 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pln:\*  
 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1804	100.0	1804	6	BD235885	BD235885	Alzheimer
2	1804	100.0	1804	6	AR224092	AR224092	Sequence
3	1804	100.0	1804	6	AR269223	AR269223	Sequence
4	1804	100.0	1804	6	AX105383	AX105383	Sequence
5	1804	100.0	1804	6	AX573821	AX573821	Sequence
6	1804	100.0	1804	9	AF200342	AF200342	Homo sapi
7	1790.6	99.3	2990	9	AF178532	AF178532	Homo sapi
8	1788.2	99.1	1885	9	AF200192	AF200192	Homo sapi
9	1784.4	98.9	1879	6	AX376004	AX376004	Sequence
10	1784.4	98.9	1879	9	AY358927	AY358927	Homo sapi
11	1768.2	98.0	1864	9	BC014453	BC014453	Homo sapi
12	1768.2	98.0	1873	6	BD231786	BD231786	Metastati
13	1768.2	98.0	1873	6	AR411231	AR411231	Sequence
14	1768.2	98.0	1873	9	AF117892	AF117892	Homo sapi
15	1765.6	97.9	1862	6	AR136909	AR136909	Sequence
16	1765.6	97.9	1862	6	E30679	E30679	ASP1. 6/200
17	1765.6	97.9	1862	6	AX775211	AX775211	Sequence
18	1765.6	97.9	1862	6	BD165905	BD165905	ASP1. 1/2
19	1765.6	97.9	1862	9	AF204944	AF204944	Homo sapi
20	1753.4	97.2	1863	6	AX351516	AX351516	Sequence
21	1753.4	97.2	1863	9	AF050171	AF050171	Homo sapi
22	1550	85.9	1621	9	AF212252	AF212252	Homo sapi
23	1483.6	82.2	1712	6	AX136403	AX136403	Sequence
24	1483.6	82.2	1712	6	BD123654	BD123654	Secretory
25	1483.6	82.2	1712	9	AK075539	AK075539	Homo sapi
26	1482.2	82.2	2840	9	AF188276	AF188276	Homo sapi
27	1478.6	82.0	2429	6	BD231769	BD231769	Metastati
28	1478.6	82.0	2429	6	AR411214	AR411214	Sequence
29	1442.6	80.0	2821	9	AF188277	AF188277	Homo sapi
30	1263.2	70.0	1494	6	AX879009	AX879009	Sequence
31	1263.2	70.0	1494	6	BD157592	BD157592	Primer fo
32	1263.2	70.0	1494	9	AK027376	AK027376	Homo sapi
33	1179.4	65.4	1774	10	AF216310	AF216310	Mus muscu

34	1134.2	62.9	1545	6	AR170159	AR170159 Sequence
35	1134.2	62.9	1545	6	AR201145	AR201145 Sequence
36	1104.6	61.2	2514	6	AR263854	AR263854 Sequence
37	953.6	52.9	1021	6	AR263907	AR263907 Sequence
38	634.6	35.2	3516	5	BC059963	BC059963 Xenopus l
39	625.2	34.7	2568	5	BC055989	BC055989 Xenopus l
40	619.6	34.3	972	10	AF051150	AF051150 Mus muscu
41	568.6	31.5	845	6	AX866692	AX866692 Sequence
42	568.6	31.5	845	6	BD146754	BD146754 Primer fo
c 43	496	27.5	554	6	AX136731	AX136731 Sequence
c 44	496	27.5	554	6	BD123971	BD123971 Secretory
45	494	27.4	45566	9	HS44C5	AL773570 Homo sapi

# ALIGNMENTS

## RESULT 1

BD235885

LOCUS BD235885 1804 bp DNA linear PAT 17-JUL-2003

DEFINITION Alzheimer's disease secretase.

ACCESSION BD235885

VERSION BD235885.1 GI:33045655

KEYWORDS JP 2002526081-A/1.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1804)

AUTHORS Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and Yan,R.

TITLE Alzheimer's disease secretase

JOURNAL Patent: JP 2002526081-A 1 20-AUG-2002;

PHARMACIA AND UPJOHN CO

COMMENT OS Homo sapiens (human)

PN JP 2002526081-A/1

PD 20-AUG-2002

PF 23-SEP-1999 JP 2000574268

PR 24-SEP-1998 US 60/101594

PI MARK E GURNEY,MICHAEL JEROME BIENKOWSKI,ROBERT LEROY PI HEINRIKSON,

PI LUIS A PARODI,RIQIANG YAN

PC C12N15/09,A61K45/00,A61P25/28,C07K14/47,C07K16/18,C12N1/15, PC C12N1/19,

PC

C12N1/21,C12N5/10,C12N9/64,C12P21/02,C12P21/08,C12Q1/37,G01N33/ PC 15,

PC G01N33/50//(C12N1/21,C12R1:19),C12N15/00,C12N5/00 CC

Alzheimer's disease secretase

FH Key Location/Qualifiers

FT source 1. .1804

FT /organism='Homo sapiens (human) '.

FEATURES Location/Qualifiers

source 1. .1804

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 1804; DB 6; Length 1804;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780

Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620

```

Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1680
          |||
Db      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1680

Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          |||
Db      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAAAA 1800
          |||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAAAA 1800

Qy      1801 AAAA 1804
          |||
Db      1801 AAAA 1804

```

## RESULT 2

AR224092

LOCUS AR224092 1804 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 1 from patent US 6440698.

ACCESSION AR224092

VERSION AR224092.1 GI:23332752

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1804)

AUTHORS Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and Yan,R.

TITLE Alzheimer's disease secretase, APP substrates therefor, and uses therefor

JOURNAL Patent: US 6440698-A 1 27-AUG-2002;

FEATURES Location/Qualifiers

source 1. .1804

/organism="unknown"

/mol\_type="genomic DNA"

## ORIGIN

Query Match 100.0%; Score 1804; DB 6; Length 1804;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
          |||
Db      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
          |||
Db      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy      121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
          |||
Db      121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
          |||

```

Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080



Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAATAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAATAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

RESULT 3  
 AR269223  
 LOCUS

AR269223

1804 bp

DNA

linear

PAT 10-APR-2003

DEFINITION Sequence 1 from patent US 6500667.  
 ACCESSION AR269223  
 VERSION AR269223.1 GI:29700191  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 1804)  
 AUTHORS Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and Yan,R.  
 TITLE Aspartyl protease 2 (Asp2) antisense oligonucleotides  
 JOURNAL Patent: US 6500667-A 1 31-DEC-2002;  
 FEATURES Location/Qualifiers  
     source 1. .1804  
             /organism="unknown"  
             /mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 1804; DB 6; Length 1804;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540

Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380

Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA	1800
Qy	1801	AAAA	1804
Db	1801	AAAA	1804

#### RESULT 4

AX105383

LOCUS AX105383 1804 bp DNA linear PAT 30-APR-2001

DEFINITION Sequence 1 from Patent WO0123533.

ACCESSION AX105383

VERSION AX105383.1 GI:13921510

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Gurney,M. and Bienkowski,M.J.

TITLE Alzheimer's disease secretase, app substrates therefor, and uses therefor

JOURNAL Patent: WO 0123533-A 1 05-APR-2001; Pharmacia & Upjohn Company (US)

FEATURES Location/Qualifiers

source 1. .1804

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 1804; DB 6; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840

Db	781	 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCTCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCTCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680





Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080

Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

RESULT 6  
 AF200342  
 LOCUS

AF200342

1804 bp

mRNA

linear

PRI 12-DEC-1999

DEFINITION Homo sapiens chromosome 21 aspartyl protease 1 mRNA, complete cds.  
 ACCESSION AF200342  
 VERSION AF200342.1 GI:6561811  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1804)  
 AUTHORS Yan,R., Bienkowski,M.J., Shuck,M.E., Miao,H., Tory,M.C.,  
 Pauley,A.M., Brashier,J.R., Stratman,N.C., Mathews,W.R., Buhl,A.E.,  
 Carter,D.B., Tomasselli,A.G., Parodi,L.A., Heinrikson,R.L. and  
 Gurney,M.E.  
 TITLE Membrane-anchored aspartyl protease with Alzheimer's disease  
 beta-secretase activity  
 JOURNAL Nature 402 (6761), 533-537 (1999)  
 MEDLINE 20057170  
 PUBMED 10591213  
 REFERENCE 2 (bases 1 to 1804)  
 AUTHORS Bienkowski,M.J., Shuck,M.E., Slightom,J.L. and Drong,R.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-OCT-1999) Genomics Research, Pharmacia&Upjohn, 301  
 Henrietta, Kalamazoo, MI 49007, USA  
 FEATURES Location/Qualifiers  
 source 1. .1804  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /chromosome="21"  
 CDS 1. .1557  
 /codon\_start=1  
 /product="aspartyl protease 1"  
 /protein\_id="AAF17078.1"  
 /db\_xref="GI:6561812"  
 /translation="MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVA  
 PTPGPGTPAERHADGLALALEPALASPAGAANFLAMVDNLQDSGRGYYLEMLIGTPP  
 QKLQILVDTGSSNFAVAGTPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGE  
 DLVTIPKGFNTSFLVNIATIFESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDSL  
 VTQANIIPNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQI  
 EILKLEIGGQSLNLDREYNADKAIVDSGTLLRLPQKVFDVAVVEAVARASLIPEFSD  
 GFWTGSQLACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPQLYIQPMMGAGLNYE  
 CYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAEIAGA AVSEISGPFST  
 EDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLLVLLLLPFRRCQRRPRDPEVVND  
 ESSLVRRHWK"

# ORIGIN

Query Match 100.0%; Score 1804; DB 9; Length 1804;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120

Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960

Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCTCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCTCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA	1804



Db 1801 AAAA 1804

RESULT 7

AF178532

LOCUS AF178532 2990 bp mRNA linear PRI 21-SEP-2000

DEFINITION Homo sapiens aspartyl protease (BACE2) mRNA, complete cds.

ACCESSION AF178532

VERSION AF178532.1 GI:6851265

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2990)

AUTHORS Solans,A., Estivill,X. and de La Luna,S.

TITLE A new aspartyl protease on 21q22.3, BACE2, is highly similar to Alzheimer's amyloid precursor protein beta-secretase

JOURNAL Cytogenet. Cell Genet. 89 (3-4), 177-184 (2000)

MEDLINE 20422477

PUBMED 10965118

REFERENCE 2 (bases 1 to 2990)

AUTHORS Solans,A., Estivill,X. and de la Luna,S.

TITLE Direct Submission

JOURNAL Submitted (18-AUG-1999) Medical and Molecular Genetics Center, IRO, Avia. Castelldefels Km 2,7, L'Hospitalet de Llobregat, Barcelona 08907, Spain

FEATURES Location/Qualifiers

source

1. .2990

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/chromosome="21"

/map="21q22.3"

/clone="YAC 552A3"

gene

1. .2990

/gene="BACE2"

CDS

464. .2020

/gene="BACE2"

/codon\_start=1

/product="aspartyl protease"

/protein\_id="AAF29494.1"

/db\_xref="GI:6851266"

/translation="MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVA  
PTPGPGTPAERHADGLALALEPALASPAGAANFLAMVDNLQGDSGRGYYLEMLIGTPP  
QKLQILVDTGSSNFAVAGTPHSYIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGE  
DLVTIPKGFNTSFLVNIATIFESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDSL  
VTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIIWYTPIKEEWYYQI  
EILKLEIGGQSLNLDREYNADKAIVDSGTLLRLPQKVFDVAVVEAVARASLIPEFSD  
GFWTGSQACWTNSETPWSYFPKISIIYLRDENSRSFRITILPQLYIQPMMGAGLNYE  
CYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAIEIAGAAVSEISGPFST  
EDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLLVLLLPFRCQRRPRDPEVVND  
ESSLVRHRWK"

polyA\_signal

2225. .2231

/gene="BACE2"

polyA\_signal

2959. .2964

/gene="BACE2"

ORIGIN

Query Match 99.3%; Score 1790.6; DB 9; Length 2990;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1793; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     464 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 523

Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    524 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 583

Qy    121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    584 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 643

Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    644 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 703

Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    704 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 763

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    764 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 823

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    824 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC 883

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    884 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 943

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    944 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT 1003

Qy    541 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1004 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 1063

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1064 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 1123

Qy    661 CAAGCAAACATCCCCAACGTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1124 CAAGCAAACATCCCCAACGTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 1183

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db	1184	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	1243
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	1244	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	1303
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	1304	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	1363
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	1364	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1423
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1424	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1483
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1484	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1543
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1544	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1603
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1604	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1663
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1664	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1723
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1724	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1783
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1784	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1843
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1844	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1903
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1904	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1963
Qy	1501	CGTGACCCTGAGGTGCTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1964	CGTGACCCTGAGGTGCTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	2023
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	2024	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	2083

Qy 1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680  
 |||  
 Db 2084 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 2143  
 Qy 1681 GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740  
 |||  
 Db 2144 GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 2203  
 Qy 1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAA 1797  
 |||  
 Db 2204 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAACAGA 2260

# RESULT 8

AF200192

LOCUS AF200192 1885 bp mRNA linear PRI 16-FEB-2000

DEFINITION Homo sapiens memapsin 1 mRNA, complete cds.

ACCESSION AF200192

VERSION AF200192.1 GI:6470290

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1885)

AUTHORS Lin,X., Koelsch,G., Wu,S., Downs,D., Dashti,A. and Tang,J.

TITLE Human aspartic protease memapsin 2 cleaves the beta-secretase site  
 of beta-amyloid precursor protein

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1456-1460 (2000)

MEDLINE 20144060

PUBMED 10677483

REFERENCE 2 (bases 1 to 1885)

AUTHORS Lin,X., Koelsch,G. and Tang,J.

TITLE Direct Submission

JOURNAL Submitted (28-OCT-1999) Protein Studies Program, Oklahoma Medical  
 Research Foundation, 825 N.E. 13th Street, Oklahoma City, OK 73104,  
 USA

FEATURES Location/Qualifiers

source

1..1885

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

CDS

78..1634

/function="cleaves beta-secretase site of beta-amyloid  
 precursor protein"

/note="membrane-associated aspartic protease 1"

/codon\_start=1

/product="memapsin 1"

/protein\_id="AAF13714.1"

/db\_xref="GI:6470291"

/translation="MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVTAATNRVVA  
 PTPGPGTPAERHADGLALALEPALASPAGAANFLAMVDNLQGDSEGRGYYLEMLIGTPP  
 QKLQILVDTGSSNFAVAGTPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGE  
 DLVTIPKGFNTSFLVNIATIFESENFPLPGIKWNGILGLAYATLAKPSSSLETFDLSL  
 VTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIIWYTPIKEEWYYQI  
 EILKLEIGGQSLNLDREYNADKAIVDSGTLLRLPQKVFDVAVVEAVARASLIPEFSD

GFWTGSQLACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPQLYIQPMMGAGLNYE  
CYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAIEIAGAAVSEISGPFST  
EDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLLVLLLPFRCQRRPRDPEVND  
ESSLVRHRWK"

ORIGIN

Query Match 99.1%; Score 1788.2; DB 9; Length 1885;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1801; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	78	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	137
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	138	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGACCGCGGCCACGAAC	197
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	198	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	257
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCCATG	240
Db	258	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCCATG	317
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	318	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	377
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	378	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	437
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	438	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	497
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	498	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	557
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	558	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	617
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	618	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	677
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	678	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	737
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	738	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	797

Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	798	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	857
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	858	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	917
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	918	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	977
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	978	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1037
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1038	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1097
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1098	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1157
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1158	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1217
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Db	1218	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1277
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1278	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1337
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1338	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1397
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1398	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1457
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1458	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1517
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1518	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1577
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1578	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1637



Qy 1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620  
 |||  
 Db 1638 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1697

Qy 1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680  
 |||  
 Db 1698 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1757

Qy 1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740  
 |||  
 Db 1758 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1817

Qy 1741 CTCCCTACTTCCAAGAAAAATAATT-AAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1799  
 |||  
 Db 1818 CTCCCTACTTCCAAGAAAAACAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAA 1877

Qy 1800 AAAAA 1804  
 |||  
 Db 1878 AAAAA 1882

# RESULT 9

AX376004

LOCUS AX376004 1879 bp DNA linear PAT 01-MAR-2002

DEFINITION Sequence 71 from Patent WO0168848.

ACCESSION AX376004

VERSION AX376004.1 GI:19170395

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,  
 Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and  
 Zhang, Z.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same

JOURNAL Patent: WO 0168848-A 71 20-SEP-2001;  
 Genentech, Inc. (US)

FEATURES Location/Qualifiers

source 1. .1879  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Query Match 98.9%; Score 1784.4; DB 6; Length 1879;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60  
 |||  
 Db 94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy 61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC 120  
 |||

Db	154	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	213
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	214	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	273
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	274	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	334	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	393
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	394	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	453
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053

Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1879

## RESULT 10

AY358927

LOCUS AY358927 1879 bp mRNA linear PRI 03-OCT-2003

DEFINITION Homo sapiens clone DNA45493 BACE2 (UNQ418) mRNA, complete cds.

ACCESSION AY358927

VERSION AY358927.1 GI:37182971

KEYWORDS FLI\_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1879)

AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,  
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,  
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,  
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
Goddard,A., Wood,W.I. and Godowski,P.TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment

JOURNAL Genome Res. 13 (10), 2265-2270 (2003)

PUBMED 12975309

REFERENCE 2 (bases 1 to 1879)

AUTHORS Clark,H.F.

TITLE Direct Submission

JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES Location/Qualifiers

source

1. .1879  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DNA45493"

gene

1. .1879  
/locus\_tag="UNQ418"

CDS

94. .1650  
/locus\_tag="UNQ418"  
/note="PRO852"  
/codon\_start=1  
/product="BACE2"  
/protein\_id="AAQ89286.1"  
/db\_xref="GI:37182972"/translation="MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVA  
PTPGPGTPAERHADGLALALEPALASPAGAANFLAMVDNLQGDSEGRGYYLEMLIGTPP  
QKLQILVDTGSSNFAVAGTPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGE  
DLVTIPKGFNTSFLVNIATIFESENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSL  
VTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIIWYTPIKEEWYYQI  
EILKLEIGGQSLNLDREYNADKAIVDSGTTLRLRPQKVFDVAVEAVARASLIPEFSD  
GFWTGSQLACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPQLYIQPMMGAGLNYE  
CYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAIEIAGAAVSEISGPFST  
EDVASNCVPAQSLSEPIWIVSYALMSVCGAILLVLLVLLLLPFCRRPRDPEVVND  
ESSLVRHRWK"

ORIGIN

Query Match 98.9%; Score 1784.4; DB 9; Length 1879;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	94	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	153
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	154	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	213
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	214	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	273
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	274	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	334	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	393
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	394	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	453
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873

Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCTCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCTCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713



Qy 1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680  
 |||  
 Db 1714 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1773  
 Qy 1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740  
 |||  
 Db 1774 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1833  
 Qy 1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA 1786  
 |||  
 Db 1834 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA 1879

RESULT 11

BC014453

LOCUS BC014453 1864 bp mRNA linear PRI 04-OCT-2003

DEFINITION Homo sapiens beta-site APP-cleaving enzyme 2, transcript variant a, mRNA (cDNA clone MGC:23029 IMAGE:4868925), complete cds.

ACCESSION BC014453

VERSION BC014453.1 GI:15680203

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1864)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 1864)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

## COMMENT

Contact: MGC help desk  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
info@bcgsc.bc.ca  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo  
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven  
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline  
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,  
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,  
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 34 Row: 1 Column: 22  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 21040358.

## FEATURES

	Location/Qualifiers
source	1. .1864 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:23029 IMAGE:4868925" /tissue_type="Skin, melanotic melanoma, high MDR." /clone_lib="NIH_MGC_49" /lab_host="DH10B-R" /note="Vector: pOTB7"
gene	1. .1864 /gene="BACE2" /note="synonyms: DRAP, ALP56, AEPLC, CEAP1, ASP1, ASP21, BAE2, CDA13" /db_xref="LocusID:25825" /db_xref="MIM:605668"
CDS	92. .1648 /codon_start=1 /product="beta-site APP-cleaving enzyme 2, isoform A preproprotein" /protein_id="AAH14453.1" /db_xref="GI:15680204" /db_xref="LocusID:25825" /translation="MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVA PTPGPGTPAERHADGLALALEPALASPAGAANFLAMVDNLQGDSEGRGYYLEMLIGTTP QKLQILVDTGSSNFAVAGTPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGE DLVTIPKGFNTSFLVNIATIFESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDSL VTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIIWYTPIKEEWYYQI EILKLEIGGQSLNLDREYNADKAIVDSGTLLRLPQKVFDAVVEAVARASLIPEFSD GFWTGSQACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPQLYIQPMMGAGLNYE CYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAETIAGAAVSEISGPFST EDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLLVLLLLLPFRCQRRPRDPEVND ESSLVRHRWK"
misc_feature	362. .1381 /note="asp; Region: Eukaryotic aspartyl protease. Aspartyl

(acid) proteases include pepsins, cathepsins, and renins. Two-domain structure, probably arising from ancestral duplication. This family does not include the retroviral nor retrotransposon proteases (pfam00077), which are much smaller and appear to be homologous to a single domain of the eukaryotic asp proteases"  
/db\_xref="CDD:pfam00026"

#### ORIGIN

Query Match 98.0%; Score 1768.2; DB 9; Length 1864;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1770; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	92	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	151
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	152	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	211
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	212	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	271
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCATG	240
Db	272	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCATG	331
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	332	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	391
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	392	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	451
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACGCTCC	420
Db	452	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACGCTCC	511
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	512	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	571
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	572	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	631
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	632	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	691
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	692	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	751

Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	752	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	811
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	812	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	871
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	872	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	931
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	932	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	991
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	992	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1051
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1052	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1111
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1112	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1171
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1172	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1231
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1232	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1291
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1292	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1351
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1352	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1411
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1412	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1471
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1472	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1531
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1532	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1591
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560

```

          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1592 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1651
Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1652 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1711
Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1712 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1771
Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1772 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1831
Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAA 1773
          |||||||||||||||||| || ||||||||
Db      1832 CTCCCTACTTCCAAGAAAAAAAATAAAAAAAA 1864

```

RESULT 12

BD231786

LOCUS BD231786 1873 bp DNA linear PAT 17-JUL-2003

DEFINITION Metastatic breast and colon cancer regulated genes.

ACCESSION BD231786

VERSION BD231786.1 GI:33041556

KEYWORDS JP 2002513542-A/18.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1873)

AUTHORS Xin,H. and Giese,K.

TITLE Metastatic breast and colon cancer regulated genes

JOURNAL Patent: JP 2002513542-A 18 14-MAY-2002;  
CHIRON CORP

COMMENT OS Homo sapiens (human)

PN JP 2002513542-A/18

PD 14-MAY-2002

PF 24-DEC-1998 JP 2000526659

PR 31-DEC-1997 US 60/070112

PI HONG XIN,KLAUSE GIESE

PC C12N15/00,C07K14/47,C07K16/18,C07K19/00,C12N9/64,C12N15/09, PC  
C12Q1/68,

PC G01N33/50//A61K45/00,A61P35/04,C12N15/00,C12N15/00 CC

Metastatic breast and colon cancer regulated genes FH Key

Location/Qualifiers

FT source 1. .1873

FT /organism='Homo sapiens (human)'.

FEATURES Location/Qualifiers

source 1. .1873

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 98.0%; Score 1768.2; DB 6; Length 1873;

Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1770; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
      |||
Db     101 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 160

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
      |||
Db     161 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 220

Qy     121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
      |||
Db     221 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 280

Qy     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
      |||
Db     281 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 340

Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
      |||
Db     341 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 400

Qy     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
      |||
Db     401 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 460

Qy     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC 420
      |||
Db     461 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC 520

Qy     421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
      |||
Db     521 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 580

Qy     481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
      |||
Db     581 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 640

Qy     541 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
      |||
Db     641 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 700

Qy     601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
      |||
Db     701 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 760

Qy     661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
      |||
Db     761 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 820

Qy     721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
      |||
Db     821 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 880

Qy     781 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
      |||
```



Db	881	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	940
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	941	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	1000
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	1001	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1060
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1061	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1120
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1121	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1180
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1181	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1240
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1241	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1300
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1301	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1360
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1361	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1420
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1421	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1480
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1481	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1540
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1541	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1600
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1601	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1660
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1661	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1720
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1721	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1780

```

Qy      1681 GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          |||
Db      1781 GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1840

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAA 1773
          |||
Db      1841 CTCCCTACTTCCAAGAAAAAAAATAAAAAAAA 1873

```

# RESULT 13

AR411231

LOCUS AR411231 1873 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 18 from patent US 6635748.

ACCESSION AR411231

VERSION AR411231.1 GI:40163285

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1873)

AUTHORS Xin,H. and Giese,K.

TITLE Metastatic breast and colon cancer regulated genes

JOURNAL Patent: US 6635748-A 18 21-OCT-2003;

FEATURES Location/Qualifiers

source 1. .1873

/organism="unknown"

/mol\_type="genomic DNA"

## ORIGIN

Query Match 98.0%; Score 1768.2; DB 6; Length 1873;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1770; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
          |||
Db      101 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 160

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
          |||
Db      161 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 220

Qy      121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
          |||
Db      221 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 280

Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
          |||
Db      281 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 340

Qy      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
          |||
Db      341 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 400

Qy      301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
          |||
Db      401 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 460

```

Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	461	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	520
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	521	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	580
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	581	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	640
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	641	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	700
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	701	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	760
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	761	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	820
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	821	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	880
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	881	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	940
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	941	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	1000
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	1001	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1060
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1061	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1120
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1121	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1180
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1181	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1240
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1241	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1300

Qy 1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260  
 |||  
 Db 1301 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1360

Qy 1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320  
 |||  
 Db 1361 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1420

Qy 1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380  
 |||  
 Db 1421 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1480

Qy 1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440  
 |||  
 Db 1481 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1540

Qy 1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC 1500  
 |||  
 Db 1541 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC 1600

Qy 1501 CGTGACCCTGAGGTGTCATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560  
 |||  
 Db 1601 CGTGACCCTGAGGTGTCATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1660

Qy 1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620  
 |||  
 Db 1661 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1720

Qy 1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1680  
 |||  
 Db 1721 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1780

Qy 1681 GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740  
 |||  
 Db 1781 GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1840

Qy 1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAA 1773  
 |||  
 Db 1841 CTCCCTACTTCCAAGAAAAAAAATAATTAAAAAAA 1873

# RESULT 14

AF117892

LOCUS AF117892 1873 bp mRNA linear PRI 14-JUL-2000

DEFINITION Homo sapiens aspartic-like protease mRNA, complete cds.

ACCESSION AF117892

VERSION AF117892.1 GI:5565865

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1873)

AUTHORS Xin,H., Stephans,J.C., Duan,X., Harrowe,G., Kim,E., Grieshammer,U.,  
 Kingsley,C. and Giese,K.

TITLE Identification of a novel aspartic-like protease differentially  
 expressed in human breast cancer cell lines

JOURNAL Biochim. Biophys. Acta 1501 (2-3), 125-137 (2000)  
 MEDLINE 20298348  
 PUBMED 10838186  
 REFERENCE 2 (bases 1 to 1873)  
 AUTHORS Xin,H., Stephans,J.C., Duan,X., Harrowe,G., Kim,E., Grieshammer,U.  
 and Giese,K.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-JAN-1999) Technologies, Chiron Co., 4560 Horton St.,  
 4.5103, Emeryville, CA 94608, USA  
 FEATURES Location/Qualifiers  
     source 1. .1873  
         /organism="Homo sapiens"  
         /mol\_type="mRNA"  
         /db\_xref="taxon:9606"  
         /cell\_type="stroma"  
         /tissue\_type="bone marrow"  
     CDS 101. .1657  
         /codon\_start=1  
         /product="aspartic-like protease"  
         /protein\_id="AAD45240.1"  
         /db\_xref="GI:5565866"  
         /translation="MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVA  
         PTPGPGTPAERHADGLALALEPALASPAGAANFLAMVDNLQDSDGRGYYLEMLIGTPP  
         QKLQILVDTGSSNFAVAGTPHSYIDTYFDTERSSTYRSKGFDTVKYTGGSWTGFVGE  
         DLVTIPKGFNTSFLVNIATIFESENFLLPGIKWNGILGLAYATLAKPSSSLETFDSDL  
         VTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQI  
         EILKLEIGGQSLNLDREYNADKAIVDSGTTLRLRPQKVFDAVVEAVARASLIPEFSD  
         GFWTGSQACWTNSETPWSYFPKISYLRDENSSRSFRITILPQLYIQPMMGAGLNYE  
         CYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAIEIAGAAVSEISGPFST  
         EDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLLVLLLLPFRCQRRPRDPEVND  
         ESSLVRHRWK"

# ORIGIN

Query Match 98.0%; Score 1768.2; DB 9; Length 1873;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1770; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	101	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	160
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	161	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	220
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	221	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	280
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	281	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	340
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	341	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	400

Qy	301	CCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	401	CCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	460
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	461	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	520
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	521	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	580
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	581	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	640
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	641	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	700
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	701	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	760
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	761	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	820
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	821	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	880
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	881	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	940
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	941	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	1000
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	1001	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1060
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1061	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1120
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1121	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1180
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1181	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1240
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200



```

      |||
Db      1241 ATTCAGCCCATGATGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCTCCA 1300
Qy      1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
      |||
Db      1301 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1360
Qy      1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
      |||
Db      1361 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1420
Qy      1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
      |||
Db      1421 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1480
Qy      1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA 1440
      |||
Db      1481 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA 1540
Qy      1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC 1500
      |||
Db      1541 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC 1600
Qy      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
      |||
Db      1601 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1660
Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
      |||
Db      1661 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1720
Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1680
      |||
Db      1721 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1780
Qy      1681 GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
      |||
Db      1781 GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1840
Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAA 1773
      |||
Db      1841 CTCCCTACTTCCAAGAAAAAAAATAATTAAAAAAA 1873

```

# RESULT 15

AR136909

LOCUS AR136909 1862 bp DNA linear PAT 16-JUN-2001

DEFINITION Sequence 1 from patent US 6162630.

ACCESSION AR136909

VERSION AR136909.1 GI:14478159

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1862)

AUTHORS Powell,D.J., Southan,C., Chapman,C.G. and Evans,J.R.

TITLE ASP1

JOURNAL Patent: US 6162630-A 1 19-DEC-2000;  
FEATURES Location/Qualifiers  
source 1. .1862  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 97.9%; Score 1765.6; DB 6; Length 1862;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1768; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
        |||
Db      91 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 150

Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
        |||
Db    151 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 210

Qy    121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
        |||
Db    211 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 270

Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
        |||
Db    271 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 330

Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
        |||
Db    331 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 390

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
        |||
Db    391 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 450

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC 420
        |||
Db    451 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC 510

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
        |||
Db    511 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 570

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT 540
        |||
Db    571 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT 630

Qy    541 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
        |||
Db    631 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 690

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
        |||
Db    691 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 750

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
        |||
```

Db	751	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	810
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	811	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	870
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	871	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	930
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	931	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	990
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	991	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1050
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1051	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1110
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1111	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1170
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1171	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1230
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1231	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1290
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1291	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1350
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1351	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1410
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1411	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1470
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1471	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1530
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1531	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1590
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1591	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1650

Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1651	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1710
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1711	AGCAGCCGGGATCGATGGTGGCGCTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1770
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTCAAATC	1740
Db	1771	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTCAAATC	1830
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAA	1772
Db	1831	CTCCCTACTTCCAAGAAAAAA	1862

Search completed: February 28, 2004, 05:40:18  
Job time : 6912 secs

OM nucleic - nucleic search, using sw model

Run on: February 28, 2004, 02:44:52 ; Search time 702 Seconds  
(without alignments)  
10917.022 Million cell updates/sec

Title: US-09-668-314C-1  
Perfect score: 1804  
Sequence: 1 atgggcgcactggcccgggc.....aaaccaaaaaaaaaaaaaaa 1804

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Match	Length	DB	ID	Description	
1	1804	100.0	1804	3	AAA15661	Aaa15661 Human asp	
2	1804	100.0	1804	4	AAS11701	Aas11701 DNA encod	
3	1804	100.0	1804	4	AAD17864	Aad17864 Human asp	
4	1804	100.0	1804	4	AAD13020	Aad13020 Human asp	
5	1804	100.0	1804	4	AAD06738	Aad06738 Human asp	
6	1804	100.0	1804	4	AAS11516	Aas11516 Human cDN	
7	1804	100.0	1804	6	ABL52456	Abl52456 Human Asp	

8	1784.4	98.9	1879	2	AAZ34056	Aaz34056	Human	PRO
9	1784.4	98.9	1879	3	AAC78500	Aac78500	Human	PRO
10	1784.4	98.9	1879	4	AAS45960	Aas45960	Human	DNA
11	1784.4	98.9	1879	7	ABX78563	Abx78563	Human	PRO
12	1784.4	98.9	1879	7	ACA75535	Aca75535	Novel	hum
13	1784.4	98.9	1879	7	ACA71015	Aca71015	Human	sec
14	1784.4	98.9	1879	7	ACC87543	Acc87543	Human	sec
15	1784.4	98.9	1879	7	ACC86929	Acc86929	Human	sec
16	1784.4	98.9	1879	7	ACD04102	Acd04102	Human	sec
17	1784.4	98.9	1879	7	ACA69433	Aca69433	cDNA	enco
18	1784.4	98.9	1879	7	ACA90278	Aca90278	Novel	hum
19	1784.4	98.9	1879	7	ACC89385	Acc89385	Human	sec
20	1784.4	98.9	1879	7	ACA98176	Aca98176	Novel	hum
21	1784.4	98.9	1879	7	ACA93818	Aca93818	Human	sec
22	1784.4	98.9	1879	7	ACD15211	Acd15211	Human	sec
23	1784.4	98.9	1879	7	ACD08798	Acd08798	Human	sec
24	1784.4	98.9	1879	7	ACC96718	Acc96718	Human	sec
25	1784.4	98.9	1879	7	ACF15439	Acf15439	Human	sec
26	1784.4	98.9	1879	7	ACD42589	Acd42589	Novel	hum
27	1784.4	98.9	1879	7	ACA72806	Aca72806	Human	PRO
28	1784.4	98.9	1879	7	ACD02978	Acd02978	Novel	hum
29	1784.4	98.9	1879	7	ACD01793	Acd01793	Novel	hum
30	1784.4	98.9	1879	7	ACA91985	Aca91985	Novel	hum
31	1784.4	98.9	1879	7	ACA63624	Aca63624	Novel	hum
32	1784.4	98.9	1879	7	ACA89410	Aca89410	cDNA	enco
33	1784.4	98.9	1879	7	ACA73420	Aca73420	Human	sec
34	1784.4	98.9	1879	7	ACA05735	Aca05735	Human	sec
35	1784.4	98.9	1879	7	ACA66569	Aca66569	cDNA	enco
36	1784.4	98.9	1879	7	ACF20144	Acf20144	Human	sec
37	1784.4	98.9	1879	7	ACF19530	Acf19530	Human	sec
38	1784.4	98.9	1879	7	ACD21818	Acd21818	Human	sec
39	1784.4	98.9	1879	7	ACF12983	Acf12983	Human	sec
40	1784.4	98.9	1879	7	ACD25086	Acd25086	Human	sec
41	1784.4	98.9	1879	7	ACF00135	Acf00135	Human	sec
42	1784.4	98.9	1879	7	ACA72192	Aca72192	Novel	hum
43	1784.4	98.9	1879	7	ACD04716	Acd04716	Novel	hum
44	1784.4	98.9	1879	7	ACD18177	Acd18177	Human	sec
45	1784.4	98.9	1879	7	ACD08184	Acd08184	Human	sec

# ALIGNMENTS

## RESULT 1

AAA15661

ID AAA15661 standard; cDNA; 1804 BP.

XX

AC AAA15661;

XX

DT 03-AUG-2000 (first entry)

XX

DE Human aspartyl protease 1 (Asp1) nucleotide sequence.

XX

KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 1;

KW Alzheimer's disease; beta secretase site; ss.

XX

OS Homo sapiens.



XX  
 PN WO200017369-A2.  
 XX  
 PD 30-MAR-2000.  
 XX  
 PF 23-SEP-1999; 99WO-US020881.  
 XX  
 PR 24-SEP-1998; 98US-0101594P.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN CO.  
 XX  
 PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;  
 XX  
 DR WPI; 2000-303209/26.  
 DR P-PSDB; AAY88424.  
 XX  
 PT New enzyme designated human aspartase useful in research into Alzheimer's  
 PT Disease is capable of cleaving amyloid protein precursor at the beta  
 PT secretase site to produce amyloid beta peptide.  
 XX  
 PS Claim 11; Fig 1; 183pp; English.  
 XX  
 CC This sequence represents the human aspartyl protease nucleotide sequence.  
 CC The invention relates to a protease capable of cleaving the beta  
 CC secretase site of amyloid precursor protein (APP). The protease contains  
 CC a sequence encoding the amino acid sequence DTG and a sequence encoding  
 CC DSG or DTG separated by 100-300 amino acids. When mutated the APP gene  
 CC causes an autosomal dominant form of Alzheimer's disease. APP localises  
 CC to the cell surface membrane and have a single C-terminal transmembrane  
 CC domain. Proteolytic processing of APP produces the amyloid beta protein,  
 CC which is possibly very important in Alzheimer's disease. The invention  
 CC includes a nucleotide sequence encoding the protease, a vector containing  
 CC the nucleotide sequence, and a cell line comprising the vector. Methods  
 CC for screening for inhibitors of beta secretase activity are also given in  
 CC the invention. The human aspartase protein and nucleotide sequences and  
 CC the methods for identifying inhibitors of the protease, are useful in the  
 CC treatment of and research in to Alzheimer's disease  
 XX  
 SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 3; Length 1804;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCATG	240

Db	181	 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACCTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	 GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080

Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

ID AAS11701 standard; DNA; 1804 BP.  
XX  
AC AAS11701;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE DNA encoding human aspartyl protease 1 (Asp-1).  
XX  
KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;  
KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;  
KW beta-secretase; Alzheimer's disease; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1. .1557  
FT /\*tag= a  
FT /product= "Aspartyl protease-1 (Asp-1)"  
XX  
PN WO200149097-A2.  
XX  
PD 12-JUL-2001.  
XX  
PF 09-MAY-2001; 2001WO-IB000797.  
XX  
PR 09-MAY-2001; 2001WO-IB000797.  
XX  
PA (BIEN/) BIENKOWSKI M J.  
PA (GURN/) GURNEY M E.  
PA (HEIN/) HEINRIKSON R L.  
PA (PARO/) PARODI L A.  
PA (YANR/) YAN R.  
XX  
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;  
XX  
DR WPI; 2001-502548/55.  
DR P-PSDB; AAU07201.  
XX  
PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
PT activity.  
XX  
PS Example 2; Fig 1; 185pp; English.  
XX  
CC The invention relates to a novel purified polypeptide comprising a  
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the  
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide  
CC and the fragment retain the beta-secretase activity of the mammalian Asp2  
CC protein. Also included is an isoform of amyloid protein precursor (APP)  
CC comprising the amino acid sequence of a APP or its fragment containing an  
CC APP cleavage site recognisable by a mammalian beta-secretase, and further  
CC comprising two lysine residues at the carboxyl terminus of the amino acid  
CC sequence of the mammalian APP or APP fragment. The polypeptides are used  
CC for assaying for modulators of beta-secretase activity; identifying  
CC agents that inhibit the APP processing activity of human Asp2 aspartyl  
CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2

CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.  
CC Agents identified by the above methods are useful for treating  
CC Alzheimer's disease; and for identifying modulators of amyloid-beta  
CC (Abeta) peptide production, for use in designing therapeutics for the  
CC treatment or prevention of Alzheimer's disease. Probes and primers  
CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp  
CC nucleic acids in in vitro assays and in Northern and Southern blots. The  
CC present sequence represents the coding sequence of human Asp-1

XX

SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 4; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTAATTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTAATTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTTCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTTCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660

Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTTCAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTTCAGCGTCGCCCC	1500



Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA	1804
Db	1801	AAAA	1804

# RESULT 3

AAD17864

ID AAD17864 standard; cDNA; 1804 BP.

XX

AC AAD17864;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human aspartyl protease 1 (hu-Asp1) cDNA.

XX

KW Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;

KW chromosome 21; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	CDS	1. .1557
----	-----	----------

FT		/*tag= a
----	--	----------

FT		/product= "Human aspartyl protease 1"
----	--	---------------------------------------

FT	sig_peptide	1. .60
----	-------------	--------

FT		/*tag= b
----	--	----------

FT	mat_peptide	61. .1554
----	-------------	-----------

FT		/*tag= c
----	--	----------

FT		/product= "Mature human aspartyl protease 1"
----	--	--

XX

PN GB2357767-A.

XX

PD 04-JUL-2001.

XX

PF 22-SEP-2000; 2000GB-00023315.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA ) PHARMACIA & UPJOHN CO.

XX

PI Bienkowski MJ, Gurney M;

XX

DR WPI; 2001-444208/48.

DR P-PSDB; AAE10628.

XX

PT Polypeptide comprising fragments of human aspartyl protease with amyloid precursor protein processing activity and alpha-secretase activity, for identifying modulators useful in treating Alzheimer's disease.

XX

PS Claim 30; Fig 1; 187pp; English.

XX

CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1 proteins which lack transmembrane domain or amino terminal domain or cytoplasmic domain and retains alpha-secretase activity and amyloid protein precursor (APP) processing activity. The proteins of the invention are useful for assaying hu-Asp1 alpha-secretase activity, which in turn is useful for identifying modulators of hu-Asp1 alpha-secretase activity, where modulators that increase hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's disease (AD) which causes progressive dementia with consequent formation of amyloid plaques, neurofibrillary tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with the substrate under acidic conditions and determining the level of hu-Asp1 proteolytic activity. The present sequence is a cDNA encoding human Asp1 protein. Asp1 gene is localised on chromosome 21

XX

SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 4; Length 1804;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240

Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Db	301	CCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080

Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

RESULT 4

AAD13020

ID AAD13020 standard; cDNA; 1804 BP.

XX

AC AAD13020;  
 XX  
 DT 23-OCT-2001 (first entry)  
 XX  
 DE Human aspartyl protease 1 (Hu-Asp1) cDNA.  
 XX  
 KW Human; aspartyl protease 1; Asp 1; beta-amyloid precursor protein; APP;  
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;  
 KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;  
 KW neuroprotective; antisense therapy; gene therapy; chromosome 21; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1. .1557  
 FT /\*tag= a  
 FT /product= "Human aspartyl protease 1 (Hu-Asp1)"  
 FT sig\_peptide 1. .60  
 FT /\*tag= b  
 FT mat\_peptide 61. .1554  
 FT /\*tag= c  
 FT /product= "Mature human aspartyl protease 1 (Hu-Asp1)"  
 XX  
 PN WO200150829-A2.  
 XX  
 PD 19-JUL-2001.  
 XX  
 PF 09-MAY-2001; 2001WO-IB000799.  
 XX  
 PR 09-MAY-2001; 2001WO-IB000799.  
 XX  
 PA (BIEN/) BIENKOWSKI M J.  
 PA (GURN/) GURNEY M E.  
 PA (HEIN/) HEINRIKSON R L.  
 PA (PARO/) PARODI L A.  
 PA (YANR/) YAN R.  
 XX  
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;  
 XX  
 DR WPI; 2001-483072/52.  
 DR P-PSDB; AAE06858.  
 XX  
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
 PT activity.  
 XX  
 PS Example 2; Fig 1; 185pp; English.  
 XX  
 CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid  
 CC precursor protein (APP) isoforms and their corresponding DNA molecules.  
 CC Human aspartyl proteases can act as beta-secretase proteases useful for  
 CC treating Alzheimer's disease. APP isoforms are useful for identifying  
 CC modulators of amyloid-beta peptide production, for use in designing  
 CC therapeutics for the treatment and prevention of Alzheimer's disease,  
 CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis  
 CC and neuronal loss. APP isoforms are also used in methods for identifying

CC inhibitors and modulators of human Asp2 activity. The invention relates  
 CC to a method for identifying agents that modulate the activity of human  
 CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used  
 CC as a means to screen in cellular assays for the inhibitors of beta- and  
 CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in  
 CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-  
 CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.  
 CC The present cDNA sequence encodes human aspartyl protease 1 (Hu-Asp1). Hu  
 CC -Asp 1 gene is localised on chromosome 21

XX

SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 4; Length 1804;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660



Db	601		TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661		CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661		CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721		GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721		GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781		GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781		GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841		TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841		TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901		ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901		ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961		GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961		GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021		CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021		CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081		TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081		TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141		ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141		ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201		TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201		TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261		AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261		AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321		GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321		GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381		CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381		CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441		GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500

Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA	1804
Db	1801	AAAA	1804

# RESULT 5

AAD06738

ID AAD06738 standard; cDNA; 1804 BP.

XX

AC AAD06738;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human aspartyl protease 1 (Asp 1) cDNA.

XX

KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;

KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp 1;

KW beta-secretase; chromosome 21; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	CDS	1. .1557
----	-----	----------

FT		/*tag= a
----	--	----------

FT		/product= "Human aspartyl protease 1 (Asp 1)"
----	--	---

FT	sig_peptide	1. .60
----	-------------	--------

FT		/*tag= b
----	--	----------

FT	sig_peptide	64. .186
----	-------------	----------

FT		/*tag= c
----	--	----------

FT		/note= "Pre-pro-peptide"
----	--	--------------------------

FT	sig_peptide	67. .186
----	-------------	----------

FT		/*tag= d
----	--	----------

FT		/note= "Pro-peptide"
----	--	----------------------

FT	mat_peptide	187. .1554
----	-------------	------------

FT		/*tag= e
----	--	----------

FT /product= "Human mature aspartyl protease 1 (Asp 1)"

XX

PN WO200123533-A2.

XX

PD 05-APR-2001.

XX

PF 22-SEP-2000; 2000WO-US026080.

XX

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA ) PHARMACIA & UPJOHN CO.

XX

PI Gurney M, Bienkowski MJ;

XX

DR WPI; 2001-290516/30.

DR P-PSDB; AAE02580.

XX

PT Enzymes that cleave the alpha-secretase site of the amyloid precursor  
PT protein, useful for the treatment of Alzheimer's disease.

XX

PS Example 2; Fig 1; 189pp; English.

XX

CC The present invention relates to enzymes for cleaving the alpha-  
CC secretase site of the amyloid precursor protein (APP) and methods of  
CC identifying those enzymes. The methods may be used to identify enzymes  
CC that may be used to cleave the alpha-secretase cleavage site of the APP  
CC protein. The enzymes may be used to treat or modulate the progress of  
CC Alzheimer's disease. The present sequence is human aspartyl protease 1  
CC (Asp 1) cDNA. Asp 1 has alpha-secretase protease and beta-secretase  
CC protease activities. Asp 1 gene is located on chromosome 21

XX

SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 4; Length 1804;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

|||||

Db 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy 61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120

|||||

Db 61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy 121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

|||||

Db 121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy 181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

|||||

Db 181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy 241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Db	241	 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	 GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	 CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140

Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCTCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCTCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA	1800
Qy	1801	AAAA	1804
Db	1801	AAAA	1804

RESULT 6

AAS11516

ID AAS11516 standard; cDNA; 1804 BP.

XX

AC AAS11516;

XX

DT 24-OCT-2001 (first entry)  
 XX  
 DE Human cDNA encoding Aspartyl protease 1 (Asp1).  
 XX  
 KW Human; Aspartyl protease; Asp1; Asp2; beta-secretase; nootropic;  
 KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;  
 KW amyloid-beta; Abeta; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1. .1557  
 FT /\*tag= a  
 FT /product= "Asp1"  
 XX  
 PN WO200149098-A2.  
 XX  
 PD 12-JUL-2001.  
 XX  
 PF 09-MAY-2001; 2001WO-IB000798.  
 XX  
 PR 09-MAY-2001; 2001WO-IB000798.  
 XX  
 PA (BIEN/) BIENKOWSKI M J.  
 PA (GURN/) GURNEY M E.  
 PA (HEIN/) HEINRIKSON R L.  
 PA (PARO/) PARODI L A.  
 PA (YANR/) YAN R.  
 XX  
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;  
 XX  
 DR WPI; 2001-502549/55.  
 DR P-PSDB; AAU06602.  
 XX  
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
 PT activity.  
 XX  
 PS Example 2; Fig 1; 185pp; English.  
 XX  
 CC The invention relates to a purified polypeptide comprising a fragment of  
 CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2  
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and  
 CC the fragment retain the beta-secretase activity of the mammalian Asp2  
 CC protein. The invention also details polynucleotides for the Asp proteins  
 CC and vectors expressing them, and a polypeptide (isoform of amyloid  
 CC protein precursor (APP)) comprising the amino acid sequence of an APP or  
 CC its fragment containing an APP cleavage site recognizable by a mammalian  
 CC beta-secretase, and further comprising two lysine residues at the  
 CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP  
 CC fragment. Also included in the invention are methods of identifying  
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are  
 CC useful for treating Alzheimer's disease. APP is useful in methods for  
 CC identifying inhibitors or modulators of human Asp2 activity and amyloid-  
 CC beta (Abeta) peptide production. APP is also useful in designing  
 CC therapeutics for the treatment or prevention of Alzheimer's disease. APP



CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is  
CC associated with increased levels of Abeta processing is useful in assays  
CC relating the Alzheimer's research. The expression vector is useful for  
CC recombinantly expressing APP. Nucleic acids that hybridise to Asp  
CC oligonucleotides are useful as probes or primers. The probes are useful  
CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and  
CC Southern blots. The present sequence encodes human Asp1

XX

SQ Sequence 1804 BP; 397 A; 520 C; 458 G; 429 T; 0 U; 0 Other;

Query Match 100.0%; Score 1804; DB 4; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660

Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCTCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCTCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500

```

Qy      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
          |||
Db      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
          |||
Db      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680
          |||
Db      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          |||
Db      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA 1800
          |||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA 1800

Qy      1801 AAAA 1804
          |||
Db      1801 AAAA 1804

```

RESULT 7

ABL52456

ID ABL52456 standard; cDNA; 1804 BP.

XX

AC ABL52456;

XX

DT 16-JUL-2002 (first entry)

XX

DE Human Asp-1 nucleotide sequence SEQ ID NO:1.

XX

KW Human; Asp-1; Asp-2; aspartyl protease; enzyme; Alzheimer's disease;  
 KW proteolytic; chromosome 21; gene; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	CDS	1. .1557
FT		/*tag= a
FT		/product= "Asp-1"
FT		/note= "aspartyl protease"

XX

PN GB2367060-A.

XX

PD 27-MAR-2002.

XX

PF 29-OCT-2001; 2001GB-00025934.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.



Db	181		GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241		GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241		GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301		CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301		CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361		ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361		ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421		AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421		AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481		GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481		GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541		TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541		TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601		TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601		TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661		CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661		CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721		GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721		GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781		GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781		GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841		TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841		TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901		ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901		ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961		GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961		GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021		CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080

Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	



ID AAZ34056 standard; cDNA; 1879 BP.  
XX  
AC AAZ34056;  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Human PRO852 nucleotide sequence.  
XX  
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9946281-A2.  
XX  
PD 16-SEP-1999.  
XX  
PF 08-MAR-1999; 99WO-US005028.  
XX  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077641P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 12-MAR-1998; 98US-0077791P.  
PR 13-MAR-1998; 98US-0078004P.  
PR 17-MAR-1998; 98US-00040220.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 26-MAR-1998; 98US-0079656P.  
PR 27-MAR-1998; 98US-0079663P.  
PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079689P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 30-MAR-1998; 98US-0079920P.  
PR 30-MAR-1998; 98US-0079923P.  
PR 31-MAR-1998; 98US-0080105P.  
PR 31-MAR-1998; 98US-0080107P.  
PR 31-MAR-1998; 98US-0080165P.  
PR 31-MAR-1998; 98US-0080194P.  
PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080328P.  
PR 01-APR-1998; 98US-0080333P.  
PR 01-APR-1998; 98US-0080334P.  
PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
PR 08-APR-1998; 98US-0081071P.  
PR 09-APR-1998; 98US-0081195P.  
PR 09-APR-1998; 98US-0081203P.  
PR 09-APR-1998; 98US-0081229P.  
PR 15-APR-1998; 98US-0081817P.  
PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081952P.

PR 15-APR-1998; 98US-0081955P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082700P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082804P.  
PR 23-APR-1998; 98US-0082767P.  
PR 23-APR-1998; 98US-0082796P.  
PR 27-APR-1998; 98US-0083336P.  
PR 28-APR-1998; 98US-0083322P.  
PR 29-APR-1998; 98US-0083392P.  
PR 29-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083500P.  
PR 29-APR-1998; 98US-0083545P.  
PR 29-APR-1998; 98US-0083554P.  
PR 29-APR-1998; 98US-0083558P.  
PR 29-APR-1998; 98US-0083559P.  
PR 30-APR-1998; 98US-0083742P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 06-MAY-1998; 98US-0084441P.  
PR 07-MAY-1998; 98US-0084598P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 07-MAY-1998; 98US-0084627P.  
PR 07-MAY-1998; 98US-0084637P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 13-MAY-1998; 98US-0085323P.  
PR 13-MAY-1998; 98US-0085338P.  
PR 13-MAY-1998; 98US-0085339P.  
PR 15-MAY-1998; 98US-0085573P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085689P.  
PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 15-MAY-1998; 98US-0085704P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086392P.  
PR 22-MAY-1998; 98US-0086414P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 11-SEP-1998; 98US-0100038P.

XX

PA (GETH ) GENENTECH INC.

XX

PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX

DR WPI; 1999-551358/46.

DR P-PSDB; AAY41714.

XX

PT New secreted and transmembrane polypeptides and their polynucleotides,  
PT useful for treating blood coagulation disorders, cancers and cellular  
PT adhesion disorders.

XX

PS Claim 2; Fig 72; 530pp; English.

XX

CC The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as sources  
CC of probes, primers, for chromosome mapping, and for generation of  
CC antisense sequences. They can also be used to create transgenic animals.  
CC The proteins can be used to treat a variety of diseases and disorders,  
CC depending on their function. Diseases that may be treated include blood  
CC coagulation disorders, cancers and cellular adhesion disorders. They may  
CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to  
CC AAY41774 represent polynucleotide and polypeptide sequence given in the  
CC exemplification of the present invention

XX

SQ Sequence 1879 BP; 388 A; 559 C; 498 G; 434 T; 0 U; 0 Other;

Query Match 98.9%; Score 1784.4; DB 2; Length 1879;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCAGTGGCTCCTGCGCGCC 60  
|||||

Db 94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCAGTGGCTCCTGCGCGCC 153

Qy 61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120  
|||||

Db 154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy 121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180  
|||||

Db 214 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy 181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240  
|||||

Db 274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333

Qy 241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300  
|||||

Db 334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy 301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360  
|||||

Db 394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy 361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420  
|||||

Db 454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy 421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480  
|||||

Db 514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380

Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCAGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1879

RESULT 9

AAC78500

ID AAC78500 standard; cDNA; 1879 BP.

XX

AC AAC78500;

XX

DT 08-FEB-2001 (first entry)

XX

DE Human PRO852 (UNQ418) nucleotide sequence SEQ ID NO:195.

XX

KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
 KW expressed sequence tag; detection; cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200053756-A2.

XX

PD 14-SEP-2000.

XX

PF 18-FEB-2000; 2000WO-US004341.

XX

PR 08-MAR-1999; 99WO-US005028.

PR 12-MAR-1999; 99US-0123957P.

PR 29-MAR-1999; 99US-0126773P.

PR 21-APR-1999; 99US-0130232P.





Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	214	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	273
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	274	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	334	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	393
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	394	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	453
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053

Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1879

RESULT 10

AAS45960

ID AAS45960 standard; cDNA; 1879 BP.

XX

AC AAS45960;

XX

DT 18-DEC-2001 (first entry)

XX

DE Human DNA encoding PRO polypeptide sequence #36.

XX

KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;

KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;

KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;

KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;

KW PCR primer.

XX

OS Homo sapiens.

XX

PN WO200168848-A2.

XX

PD 20-SEP-2001.

XX

PF 28-FEB-2001; 2001WO-US006520.

XX

PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005841.

PR 03-MAR-2000; 2000US-0187202P.

PR 06-MAR-2000; 2000US-0186968P.

PR 14-MAR-2000; 2000US-0189320P.

PR 14-MAR-2000; 2000US-0189328P.

PR 15-MAR-2000; 2000WO-US006884.

PR 21-MAR-2000; 2000US-0190828P.

PR 21-MAR-2000; 2000US-0191007P.

PR 21-MAR-2000; 2000US-0191048P.

PR 21-MAR-2000; 2000US-0191314P.

PR 28-MAR-2000; 2000US-0192655P.

PR 29-MAR-2000; 2000US-0193032P.

PR 29-MAR-2000; 2000US-0193053P.

PR 30-MAR-2000; 2000WO-US008439.

PR 04-APR-2000; 2000US-0194449P.

PR 04-APR-2000; 2000US-0194647P.

PR 11-APR-2000; 2000US-0195975P.

PR 11-APR-2000; 2000US-0196000P.

PR 11-APR-2000; 2000US-0196187P.

PR 11-APR-2000; 2000US-0196690P.

PR 11-APR-2000; 2000US-0196820P.

PR 18-APR-2000; 2000US-0198121P.

PR 18-APR-2000; 2000US-0198585P.

PR 25-APR-2000; 2000US-0199397P.

PR 25-APR-2000; 2000US-0199550P.

PR 25-APR-2000; 2000US-0199654P.

PR 03-MAY-2000; 2000US-0201516P.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.

PR 05-JUN-2000; 2000US-0209832P.

PR 28-JUL-2000; 2000WO-US020710.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.

XX

PA (GETH ) GENENTECH INC.

XX

PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2001-602746/68.

DR P-PSDB; AAU29059.

XX

PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
PT presence of tumors, such as prostate and breast tumors, in mammals and to  
PT screen for modulators of the compounds.

XX

PS Claim 2; Fig 71; 774pp; English.

XX

CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR  
CC primers for PRO polypeptides of the invention. The sequences of the  
CC invention can be used to detect the presence of a tumour in a mammal by  
CC comparing the level of expression of a PRO polypeptide in a test sample  
CC of cells from the animal and a control sample of normal cells, whereby a  
CC higher level of expression in the test sample indicates the presence of a  
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,  
CC pigs, goats and rabbits but are preferably human. The polypeptides can be  
CC used to stimulate tumour necrosis factor (TNF) alpha release from human  
CC blood, when contacted with it. A specific polypeptide can be used to  
CC stimulate the proliferation or differentiation of chondrocyte cells. The  
CC PRO proteins can be used to determine the presence of tumours and also  
CC susceptibility to tumour development, particularly adrenal, lung, colon,  
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
CC can be used for genetic analysis of individuals with genetic disorders

XX

SQ Sequence 1879 BP; 388 A; 559 C; 498 G; 434 T; 0 U; 0 Other;

Query Match 98.9%; Score 1784.4; DB 4; Length 1879;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60  
|||||  
Db 94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153  
  
Qy 61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120  
|||||  
Db 154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213  
  
Qy 121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180  
|||||  
Db 214 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273  
  
Qy 181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCCATG 240

Db	274	 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	334	 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	393
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	394	 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	453
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	454	 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	 GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080

Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCAGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1879

RESULT 11

ABX78563

ID ABX78563 standard; cDNA; 1879 BP.

XX

AC ABX78563;

XX



DT 15-APR-2003 (first entry)  
 XX  
 DE Human PRO polynucleotide #36.  
 XX  
 KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;  
 KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;  
 KW antibody-dependent enzyme mediated prodrug therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003027272-A1.  
 XX  
 PD 06-FEB-2003.  
 XX  
 PF 21-JUN-2002; 2002US-00176492.  
 XX  
 PR 18-SEP-1997; 97US-0059263P.  
 PR 18-SEP-1997; 97US-0059266P.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 21-OCT-1997; 97US-0063486P.  
 PR 24-OCT-1997; 97US-0063120P.  
 PR 24-OCT-1997; 97US-0063121P.  
 PR 28-OCT-1997; 97US-0063540P.  
 PR 28-OCT-1997; 97US-0063541P.  
 PR 28-OCT-1997; 97US-0063544P.  
 PR 28-OCT-1997; 97US-0063564P.  
 PR 29-OCT-1997; 97US-0063734P.  
 PR 31-OCT-1997; 97US-0063870P.  
 PR 31-OCT-1997; 97US-0064103P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 21-NOV-1997; 97US-0066120P.  
 PR 24-NOV-1997; 97US-0066466P.  
 PR 24-NOV-1997; 97US-0066772P.  
 PR 11-DEC-1997; 97US-0069335P.  
 PR 12-DEC-1997; 97US-0069425P.  
 PR 17-DEC-1997; 97US-0069870P.  
 PR 18-DEC-1997; 97US-0068017P.  
 PR 10-MAR-1998; 98US-0077450P.  
 PR 11-MAR-1998; 98US-0077632P.  
 PR 11-MAR-1998; 98US-0077649P.  
 PR 20-MAR-1998; 98US-0078886P.  
 PR 20-MAR-1998; 98US-0078939P.  
 PR 27-MAR-1998; 98US-0079664P.  
 PR 27-MAR-1998; 98US-0079786P.  
 PR 31-MAR-1998; 98US-0080107P.  
 PR 31-MAR-1998; 98US-0080194P.  
 PR 01-APR-1998; 98US-0080327P.  
 PR 01-APR-1998; 98US-0080333P.  
 PR 08-APR-1998; 98US-0081049P.  
 PR 08-APR-1998; 98US-0081070P.  
 PR 09-APR-1998; 98US-0081195P.  
 PR 15-APR-1998; 98US-0081838P.  
 PR 21-APR-1998; 98US-0082568P.  
 PR 21-APR-1998; 98US-0082569P.  
 PR 22-APR-1998; 98US-0082704P.  
 PR 22-APR-1998; 98US-0082797P.  
 PR 28-APR-1998; 98US-0083322P.

PR	29-APR-1998;	98US-0083495P.
PR	29-APR-1998;	98US-0083496P.
PR	29-APR-1998;	98US-0083499P.
PR	29-APR-1998;	98US-0083559P.
PR	05-MAY-1998;	98US-0084366P.
PR	06-MAY-1998;	98US-0084414P.
PR	07-MAY-1998;	98US-0084639P.
PR	07-MAY-1998;	98US-0084640P.
PR	07-MAY-1998;	98US-0084643P.
PR	15-MAY-1998;	98US-0085579P.
PR	15-MAY-1998;	98US-0085580P.
PR	15-MAY-1998;	98US-0085582P.
PR	15-MAY-1998;	98US-0085700P.
PR	18-MAY-1998;	98US-0086023P.
PR	22-MAY-1998;	98US-0086392P.
PR	22-MAY-1998;	98US-0086486P.
PR	28-MAY-1998;	98US-0087098P.
PR	28-MAY-1998;	98US-0087208P.
PR	02-JUN-1998;	98US-0087609P.
PR	02-JUN-1998;	98US-0087759P.
PR	03-JUN-1998;	98US-0087827P.
PR	04-JUN-1998;	98US-0088025P.
PR	04-JUN-1998;	98US-0088028P.
PR	04-JUN-1998;	98US-0088029P.
PR	04-JUN-1998;	98US-0088033P.
PR	04-JUN-1998;	98US-0088326P.
PR	05-JUN-1998;	98US-0088167P.
PR	05-JUN-1998;	98US-0088202P.
PR	05-JUN-1998;	98US-0088212P.
PR	05-JUN-1998;	98US-0088217P.
PR	09-JUN-1998;	98US-0088655P.
PR	10-JUN-1998;	98US-0088722P.
PR	10-JUN-1998;	98US-0088738P.
PR	10-JUN-1998;	98US-0088740P.
PR	10-JUN-1998;	98US-0088811P.
PR	10-JUN-1998;	98US-0088824P.
PR	10-JUN-1998;	98US-0088825P.
PR	10-JUN-1998;	98US-0088826P.
PR	11-JUN-1998;	98US-0088861P.
PR	11-JUN-1998;	98US-0088863P.
PR	11-JUN-1998;	98US-0088876P.
PR	12-JUN-1998;	98US-0089090P.
PR	12-JUN-1998;	98US-0089105P.
PR	16-JUN-1998;	98US-0089512P.
PR	16-JUN-1998;	98US-0089514P.
PR	17-JUN-1998;	98US-0089538P.
PR	17-JUN-1998;	98US-0089598P.
PR	17-JUN-1998;	98US-0089653P.
PR	18-JUN-1998;	98US-0089908P.
PR	19-JUN-1998;	98US-0089952P.
PR	22-JUN-1998;	98US-0090246P.
PR	22-JUN-1998;	98US-0090252P.
PR	22-JUN-1998;	98US-0090254P.
PR	24-JUN-1998;	98US-0090429P.
PR	24-JUN-1998;	98US-0090435P.
PR	24-JUN-1998;	98US-0090444P.
PR	24-JUN-1998;	98US-0090461P.

PR 24-JUN-1998; 98US-0090535P.  
PR 24-JUN-1998; 98US-0090540P.  
PR 25-JUN-1998; 98US-0090676P.  
PR 25-JUN-1998; 98US-0090678P.  
PR 25-JUN-1998; 98US-0090688P.  
PR 25-JUN-1998; 98US-0090690P.  
PR 25-JUN-1998; 98US-0090694P.  
PR 25-JUN-1998; 98US-0090695P.  
PR 25-JUN-1998; 98US-0090696P.  
PR 26-JUN-1998; 98US-00105413.  
PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 26-JUN-1998; 98US-0091010P.  
PR 01-JUL-1998; 98US-0091359P.  
PR 01-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091478P.  
PR 02-JUL-1998; 98US-0091486P.  
PR 02-JUL-1998; 98US-0091626P.  
PR 02-JUL-1998; 98US-0091628P.  
PR 02-JUL-1998; 98US-0091632P.  
PR 24-JUL-1998; 98US-0094006P.  
PR 04-AUG-1998; 98US-0095282P.  
PR 10-AUG-1998; 98US-0095998P.  
PR 10-AUG-1998; 98US-0096012P.  
PR 17-AUG-1998; 98US-0096757P.  
PR 17-AUG-1998; 98US-0096766P.  
PR 17-AUG-1998; 98US-0096867P.  
PR 17-AUG-1998; 98US-0096891P.  
PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096959P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.  
PR 26-AUG-1998; 98US-0097955P.  
PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 01-SEP-1998; 98US-0098716P.  
PR 01-SEP-1998; 98US-0098723P.  
PR 02-SEP-1998; 98US-0098803P.  
PR 02-SEP-1998; 98US-0098821P.  
PR 02-SEP-1998; 98US-0098843P.  
PR 09-SEP-1998; 98US-0099602P.  
PR 10-SEP-1998; 98US-0099741P.  
PR 10-SEP-1998; 98US-0099754P.  
PR 10-SEP-1998; 98US-0099763P.  
PR 10-SEP-1998; 98US-0099812P.  
PR 15-SEP-1998; 98US-0100388P.  
PR 16-SEP-1998; 98US-0100662P.  
PR 16-SEP-1998; 98US-0100664P.  
PR 16-SEP-1998; 98US-0101751P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100683P.  
PR 17-SEP-1998; 98US-0100684P.  
PR 17-SEP-1998; 98US-0100919P.  
PR 17-SEP-1998; 98US-0100930P.

PR 18-SEP-1998; 98US-0100849P.  
 PR 18-SEP-1998; 98US-0101014P.  
 PR 18-SEP-1998; 98US-0101068P.  
 PR 23-SEP-1998; 98US-0101471P.  
 PR 23-SEP-1998; 98US-0101472P.  
 PR 23-SEP-1998; 98US-0101475P.  
 PR 23-SEP-1998; 98US-0101477P.  
 PR 24-SEP-1998; 98US-0101738P.  
 PR 24-SEP-1998; 98US-0101739P.  
 PR 24-SEP-1998; 98US-0101743P.  
 PR 24-SEP-1998; 98US-0101922P.  
 PR 25-SEP-1998; 98US-0101786P.  
 PR 29-SEP-1998; 98US-0102207P.  
 PR 29-SEP-1998; 98US-0102240P.  
 PR 29-SEP-1998; 98US-0102330P.  
 PR 29-SEP-1998; 98US-0102331P.  
 PR 30-SEP-1998; 98US-0102487P.  
 PR 30-SEP-1998; 98US-0102570P.  
 PR 30-SEP-1998; 98US-0102571P.  
 PR 01-OCT-1998; 98US-0102684P.  
 PR 01-OCT-1998; 98US-0102687P.  
 PR 02-OCT-1998; 98US-0102965P.  
 PR 06-OCT-1998; 98US-0103258P.  
 PR 06-OCT-1998; 98US-0103449P.  
 PR 07-OCT-1998; 98US-00168978.

Query Match 98.9%; Score 1784.4; DB 7; Length 1879;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	94	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	153
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	154	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	213
Qy	121	CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	214	CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	273
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	274	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	334	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	393
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	394	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	453
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513

Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353

Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1879

RESULT 12

ACA75535

ID ACA75535 standard; cDNA; 1879 BP.

XX

AC ACA75535;

XX

DT 07-JUL-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO852 cDNA.

XX

KW Human; secreted and transmembrane protein: PRO; gene therapy;

KW tumour necrosis factor-alpha release; TNF-alpha release;

KW chondrocyte proliferation; chondrocyte differentiation; tumour;

KW adrenal tumour; lung tumour; colon tumour; breast tumour;

KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.

XX

OS Homo sapiens.

XX

PN US2003032127-A1.

XX



PD 13-FEB-2003.  
XX  
PF 26-JUN-2002; 2002US-00183012.  
XX  
PR 18-SEP-1997; 97US-0059263P.  
PR 18-SEP-1997; 97US-0059266P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0063120P.  
PR 24-OCT-1997; 97US-0063121P.  
PR 28-OCT-1997; 97US-0063540P.  
PR 28-OCT-1997; 97US-0063541P.  
PR 28-OCT-1997; 97US-0063544P.  
PR 28-OCT-1997; 97US-0063564P.  
PR 29-OCT-1997; 97US-0063734P.  
PR 31-OCT-1997; 97US-0063870P.  
PR 31-OCT-1997; 97US-0064103P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066120P.  
PR 24-NOV-1997; 97US-0066466P.  
PR 24-NOV-1997; 97US-0066772P.  
PR 11-DEC-1997; 97US-0069335P.  
PR 12-DEC-1997; 97US-0069425P.  
PR 17-DEC-1997; 97US-0069870P.  
PR 18-DEC-1997; 97US-0068017P.  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 31-MAR-1998; 98US-0080107P.  
PR 31-MAR-1998; 98US-0080194P.  
PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080333P.  
PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
PR 09-APR-1998; 98US-0081195P.  
PR 15-APR-1998; 98US-0081838P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082797P.  
PR 28-APR-1998; 98US-0083322P.  
PR 29-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083559P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.

PR	15-MAY-1998;	98US-0085700P.
PR	18-MAY-1998;	98US-0086023P.
PR	22-MAY-1998;	98US-0086392P.
PR	22-MAY-1998;	98US-0086486P.
PR	28-MAY-1998;	98US-0087098P.
PR	28-MAY-1998;	98US-0087208P.
PR	02-JUN-1998;	98US-0087609P.
PR	02-JUN-1998;	98US-0087759P.
PR	03-JUN-1998;	98US-0087827P.
PR	04-JUN-1998;	98US-0088025P.
PR	04-JUN-1998;	98US-0088028P.
PR	04-JUN-1998;	98US-0088029P.
PR	04-JUN-1998;	98US-0088033P.
PR	04-JUN-1998;	98US-0088326P.
PR	05-JUN-1998;	98US-0088167P.
PR	05-JUN-1998;	98US-0088202P.
PR	05-JUN-1998;	98US-0088212P.
PR	05-JUN-1998;	98US-0088217P.
PR	09-JUN-1998;	98US-0088655P.
PR	10-JUN-1998;	98US-0088722P.
PR	10-JUN-1998;	98US-0088738P.
PR	10-JUN-1998;	98US-0088740P.
PR	10-JUN-1998;	98US-0088811P.
PR	10-JUN-1998;	98US-0088824P.
PR	10-JUN-1998;	98US-0088825P.
PR	10-JUN-1998;	98US-0088826P.
PR	11-JUN-1998;	98US-0088861P.
PR	11-JUN-1998;	98US-0088863P.
PR	11-JUN-1998;	98US-0088876P.
PR	12-JUN-1998;	98US-0089090P.
PR	12-JUN-1998;	98US-0089105P.
PR	16-JUN-1998;	98US-0089512P.
PR	16-JUN-1998;	98US-0089514P.
PR	17-JUN-1998;	98US-0089538P.
PR	17-JUN-1998;	98US-0089598P.
PR	17-JUN-1998;	98US-0089653P.
PR	18-JUN-1998;	98US-0089908P.
PR	19-JUN-1998;	98US-0089952P.
PR	22-JUN-1998;	98US-0090246P.
PR	22-JUN-1998;	98US-0090252P.
PR	22-JUN-1998;	98US-0090254P.
PR	24-JUN-1998;	98US-0090429P.
PR	24-JUN-1998;	98US-0090435P.
PR	24-JUN-1998;	98US-0090444P.
PR	24-JUN-1998;	98US-0090461P.
PR	24-JUN-1998;	98US-0090535P.
PR	24-JUN-1998;	98US-0090540P.
PR	25-JUN-1998;	98US-0090676P.
PR	25-JUN-1998;	98US-0090678P.
PR	25-JUN-1998;	98US-0090688P.
PR	25-JUN-1998;	98US-0090690P.
PR	25-JUN-1998;	98US-0090694P.
PR	25-JUN-1998;	98US-0090695P.
PR	25-JUN-1998;	98US-0090696P.
PR	26-JUN-1998;	98US-00105413.
PR	26-JUN-1998;	98US-0090862P.
PR	26-JUN-1998;	98US-0090863P.

PR	26-JUN-1998;	98US-0091010P.
PR	01-JUL-1998;	98US-0091359P.
PR	01-JUL-1998;	98US-0091544P.
PR	02-JUL-1998;	98US-0091478P.
PR	02-JUL-1998;	98US-0091486P.
PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091632P.
PR	24-JUL-1998;	98US-0094006P.
PR	04-AUG-1998;	98US-0095282P.
PR	10-AUG-1998;	98US-0095998P.
PR	10-AUG-1998;	98US-0096012P.
PR	17-AUG-1998;	98US-0096757P.
PR	17-AUG-1998;	98US-0096766P.
PR	17-AUG-1998;	98US-0096867P.
PR	17-AUG-1998;	98US-0096891P.
PR	17-AUG-1998;	98US-0096897P.
PR	18-AUG-1998;	98US-0096949P.
PR	18-AUG-1998;	98US-0096959P.
PR	18-AUG-1998;	98US-0097022P.
PR	26-AUG-1998;	98US-0097952P.
PR	26-AUG-1998;	98US-0097954P.
PR	26-AUG-1998;	98US-0097955P.
PR	26-AUG-1998;	98US-0097971P.
PR	26-AUG-1998;	98US-0097974P.
PR	26-AUG-1998;	98US-0098014P.
PR	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098723P.
PR	02-SEP-1998;	98US-0098803P.
PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
PR	09-SEP-1998;	98US-0099602P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099812P.
PR	15-SEP-1998;	98US-0100388P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	16-SEP-1998;	98US-0101751P.
PR	16-SEP-1998;	98WO-US019330.
PR	17-SEP-1998;	98US-0100683P.
PR	17-SEP-1998;	98US-0100684P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101477P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101739P.
PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101922P.
PR	25-SEP-1998;	98US-0101786P.

PR 29-SEP-1998; 98US-0102207P.  
PR 29-SEP-1998; 98US-0102240P.  
PR 29-SEP-1998; 98US-0102330P.  
PR 29-SEP-1998; 98US-0102331P.  
PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.  
PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103258P.

Query Match 98.9%; Score 1784.4; DB 7; Length 1879;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60  
|||||  
Db 94 ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy 61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120  
|||||  
Db 154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy 121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180  
|||||  
Db 214 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy 181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240  
|||||  
Db 274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333

Qy 241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300  
|||||  
Db 334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy 301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360  
|||||  
Db 394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy 361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420  
|||||  
Db 454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy 421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480  
|||||  
Db 514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

Qy 481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540  
|||||  
Db 574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633

Qy 541 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600  
|||||  
Db 634 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy 601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660

Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGCATTTCCCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGCATTTCCCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500

Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGTCAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1879

RESULT 13

ACA71015

ID ACA71015 standard; cDNA; 1879 BP.

XX

AC ACA71015;

XX

DT 02-AUG-2003 (first entry)

XX

DE Human secreted/transmembrane protein (PRO) cDNA #36.

XX

KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;  
 KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
 KW tissue typing.

XX

OS Homo sapiens.

XX

PN US2003032112-A1.

XX

PD 13-FEB-2003.

XX

PF 21-JUN-2002; 2002US-00176756.

XX

PR	18-SEP-1997;	97US-0059263P.
PR	18-SEP-1997;	97US-0059266P.
PR	17-OCT-1997;	97US-0062250P.
PR	21-OCT-1997;	97US-0063486P.
PR	24-OCT-1997;	97US-0063120P.
PR	24-OCT-1997;	97US-0063121P.
PR	28-OCT-1997;	97US-0063540P.
PR	28-OCT-1997;	97US-0063541P.
PR	28-OCT-1997;	97US-0063544P.
PR	28-OCT-1997;	97US-0063564P.
PR	29-OCT-1997;	97US-0063734P.
PR	31-OCT-1997;	97US-0063870P.



PR	31-OCT-1997;	97US-0064103P.
PR	13-NOV-1997;	97US-0065311P.
PR	21-NOV-1997;	97US-0066120P.
PR	24-NOV-1997;	97US-0066466P.
PR	24-NOV-1997;	97US-0066772P.
PR	11-DEC-1997;	97US-0069335P.
PR	12-DEC-1997;	97US-0069425P.
PR	17-DEC-1997;	97US-0069870P.
PR	18-DEC-1997;	97US-0068017P.
PR	10-MAR-1998;	98US-0077450P.
PR	11-MAR-1998;	98US-0077632P.
PR	11-MAR-1998;	98US-0077649P.
PR	20-MAR-1998;	98US-0078886P.
PR	20-MAR-1998;	98US-0078939P.
PR	27-MAR-1998;	98US-0079664P.
PR	27-MAR-1998;	98US-0079786P.
PR	31-MAR-1998;	98US-0080107P.
PR	31-MAR-1998;	98US-0080194P.
PR	01-APR-1998;	98US-0080327P.
PR	01-APR-1998;	98US-0080333P.
PR	08-APR-1998;	98US-0081049P.
PR	08-APR-1998;	98US-0081070P.
PR	09-APR-1998;	98US-0081195P.
PR	15-APR-1998;	98US-0081838P.
PR	21-APR-1998;	98US-0082568P.
PR	21-APR-1998;	98US-0082569P.
PR	22-APR-1998;	98US-0082704P.
PR	22-APR-1998;	98US-0082797P.
PR	28-APR-1998;	98US-0083322P.
PR	29-APR-1998;	98US-0083495P.
PR	29-APR-1998;	98US-0083496P.
PR	29-APR-1998;	98US-0083499P.
PR	29-APR-1998;	98US-0083559P.
PR	05-MAY-1998;	98US-0084366P.
PR	06-MAY-1998;	98US-0084414P.
PR	07-MAY-1998;	98US-0084639P.
PR	07-MAY-1998;	98US-0084640P.
PR	07-MAY-1998;	98US-0084643P.
PR	15-MAY-1998;	98US-0085579P.
PR	15-MAY-1998;	98US-0085580P.
PR	15-MAY-1998;	98US-0085582P.
PR	15-MAY-1998;	98US-0085700P.
PR	18-MAY-1998;	98US-0086023P.
PR	22-MAY-1998;	98US-0086392P.
PR	22-MAY-1998;	98US-0086486P.
PR	28-MAY-1998;	98US-0087098P.
PR	28-MAY-1998;	98US-0087208P.
PR	02-JUN-1998;	98US-0087609P.
PR	02-JUN-1998;	98US-0087759P.
PR	03-JUN-1998;	98US-0087827P.
PR	04-JUN-1998;	98US-0088025P.
PR	04-JUN-1998;	98US-0088028P.
PR	04-JUN-1998;	98US-0088029P.
PR	04-JUN-1998;	98US-0088033P.
PR	04-JUN-1998;	98US-0088326P.
PR	05-JUN-1998;	98US-0088167P.
PR	05-JUN-1998;	98US-0088202P.

PR	05-JUN-1998;	98US-0088212P.
PR	05-JUN-1998;	98US-0088217P.
PR	09-JUN-1998;	98US-0088655P.
PR	10-JUN-1998;	98US-0088722P.
PR	10-JUN-1998;	98US-0088738P.
PR	10-JUN-1998;	98US-0088740P.
PR	10-JUN-1998;	98US-0088811P.
PR	10-JUN-1998;	98US-0088824P.
PR	10-JUN-1998;	98US-0088825P.
PR	10-JUN-1998;	98US-0088826P.
PR	11-JUN-1998;	98US-0088861P.
PR	11-JUN-1998;	98US-0088863P.
PR	11-JUN-1998;	98US-0088876P.
PR	12-JUN-1998;	98US-0089090P.
PR	12-JUN-1998;	98US-0089105P.
PR	16-JUN-1998;	98US-0089512P.
PR	16-JUN-1998;	98US-0089514P.
PR	17-JUN-1998;	98US-0089538P.
PR	17-JUN-1998;	98US-0089598P.
PR	17-JUN-1998;	98US-0089653P.
PR	18-JUN-1998;	98US-0089908P.
PR	19-JUN-1998;	98US-0089952P.
PR	22-JUN-1998;	98US-0090246P.
PR	22-JUN-1998;	98US-0090252P.
PR	22-JUN-1998;	98US-0090254P.
PR	24-JUN-1998;	98US-0090429P.
PR	24-JUN-1998;	98US-0090435P.
PR	24-JUN-1998;	98US-0090444P.
PR	24-JUN-1998;	98US-0090461P.
PR	24-JUN-1998;	98US-0090535P.
PR	24-JUN-1998;	98US-0090540P.
PR	25-JUN-1998;	98US-0090676P.
PR	25-JUN-1998;	98US-0090678P.
PR	25-JUN-1998;	98US-0090688P.
PR	25-JUN-1998;	98US-0090690P.
PR	25-JUN-1998;	98US-0090694P.
PR	25-JUN-1998;	98US-0090695P.
PR	25-JUN-1998;	98US-0090696P.
PR	26-JUN-1998;	98US-00105413.
PR	26-JUN-1998;	98US-0090862P.
PR	26-JUN-1998;	98US-0090863P.
PR	26-JUN-1998;	98US-0091010P.
PR	01-JUL-1998;	98US-0091359P.
PR	01-JUL-1998;	98US-0091544P.
PR	02-JUL-1998;	98US-0091478P.
PR	02-JUL-1998;	98US-0091486P.
PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091632P.
PR	24-JUL-1998;	98US-0094006P.
PR	04-AUG-1998;	98US-0095282P.
PR	10-AUG-1998;	98US-0095998P.
PR	10-AUG-1998;	98US-0096012P.
PR	17-AUG-1998;	98US-0096757P.
PR	17-AUG-1998;	98US-0096766P.
PR	17-AUG-1998;	98US-0096867P.
PR	17-AUG-1998;	98US-0096891P.

PR	17-AUG-1998;	98US-0096897P.
PR	18-AUG-1998;	98US-0096949P.
PR	18-AUG-1998;	98US-0096959P.
PR	18-AUG-1998;	98US-0097022P.
PR	26-AUG-1998;	98US-0097952P.
PR	26-AUG-1998;	98US-0097954P.
PR	26-AUG-1998;	98US-0097955P.
PR	26-AUG-1998;	98US-0097971P.
PR	26-AUG-1998;	98US-0097974P.
PR	26-AUG-1998;	98US-0098014P.
PR	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098723P.
PR	02-SEP-1998;	98US-0098803P.
PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
PR	09-SEP-1998;	98US-0099602P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099812P.
PR	15-SEP-1998;	98US-0100388P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	16-SEP-1998;	98US-0101751P.
PR	16-SEP-1998;	98WO-US019330.
PR	17-SEP-1998;	98US-0100683P.
PR	17-SEP-1998;	98US-0100684P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101477P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101739P.
PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101922P.
PR	25-SEP-1998;	98US-0101786P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-00168978.

Query Match 98.9%; Score 1784.4; DB 7; Length 1879;  
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
      |||
Db     94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC 120
      |||
Db    154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy    121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
      |||
Db    214 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCATG 240
      |||
Db    274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCATG 333

Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
      |||
Db    334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
      |||
Db    394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
      |||
Db    454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
      |||
Db    514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT 540
      |||
Db    574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT 633

Qy    541 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
      |||
Db    634 TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
      |||
Db    694 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 753

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
      |||
Db    754 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 813

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
      |||
Db    814 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 873

Qy    781 GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 840
      |||
Db    874 GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA 933
```

Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGCTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGCTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1773

Qy 1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740  
 |||  
 Db 1774 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1833

Qy 1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA 1786  
 |||  
 Db 1834 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA 1879

RESULT 14

ACC87543

ID ACC87543 standard; cDNA; 1879 BP.

XX

AC ACC87543;

XX

DT 05-AUG-2003 (first entry)

XX

DE Human secreted polypeptide PRO852-encoding cDNA, SEQ ID NO:71.

XX

KW Human; PRO; secreted protein; transmembrane protein;

KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;

KW chondrocyte; proliferation; differentiation; cartilage disorder;

KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;

KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;

KW liver; drug screening; transgenic animal; genetic analysis;

KW antiarthritic; vulnerary; gene therapy; gene; ss.

XX

OS Homo sapiens.

XX

PN US2003027278-A1.

XX

PD 06-FEB-2003.

XX

PF 21-JUN-2002; 2002US-00176987.

XX

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 17-OCT-1997; 97US-0062250P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 28-OCT-1997; 97US-0063540P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063734P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0066120P.

PR 24-NOV-1997; 97US-0066466P.

PR 24-NOV-1997; 97US-0066772P.

PR 11-DEC-1997; 97US-0069335P.

PR 12-DEC-1997; 97US-0069425P.

PR 17-DEC-1997; 97US-0069870P.

PR 18-DEC-1997; 97US-0068017P.

PR 10-MAR-1998; 98US-0077450P.



PR	11-MAR-1998;	98US-0077632P.
PR	11-MAR-1998;	98US-0077649P.
PR	20-MAR-1998;	98US-0078886P.
PR	20-MAR-1998;	98US-0078939P.
PR	27-MAR-1998;	98US-0079664P.
PR	27-MAR-1998;	98US-0079786P.
PR	31-MAR-1998;	98US-0080107P.
PR	31-MAR-1998;	98US-0080194P.
PR	01-APR-1998;	98US-0080327P.
PR	01-APR-1998;	98US-0080333P.
PR	08-APR-1998;	98US-0081049P.
PR	08-APR-1998;	98US-0081070P.
PR	09-APR-1998;	98US-0081195P.
PR	15-APR-1998;	98US-0081838P.
PR	21-APR-1998;	98US-0082568P.
PR	21-APR-1998;	98US-0082569P.
PR	22-APR-1998;	98US-0082704P.
PR	22-APR-1998;	98US-0082797P.
PR	28-APR-1998;	98US-0083322P.
PR	29-APR-1998;	98US-0083495P.
PR	29-APR-1998;	98US-0083496P.
PR	29-APR-1998;	98US-0083499P.
PR	29-APR-1998;	98US-0083559P.
PR	05-MAY-1998;	98US-0084366P.
PR	06-MAY-1998;	98US-0084414P.
PR	07-MAY-1998;	98US-0084639P.
PR	07-MAY-1998;	98US-0084640P.
PR	07-MAY-1998;	98US-0084643P.
PR	15-MAY-1998;	98US-0085579P.
PR	15-MAY-1998;	98US-0085580P.
PR	15-MAY-1998;	98US-0085582P.
PR	15-MAY-1998;	98US-0085700P.
PR	18-MAY-1998;	98US-0086023P.
PR	22-MAY-1998;	98US-0086392P.
PR	22-MAY-1998;	98US-0086486P.
PR	28-MAY-1998;	98US-0087098P.
PR	28-MAY-1998;	98US-0087208P.
PR	02-JUN-1998;	98US-0087609P.
PR	02-JUN-1998;	98US-0087759P.
PR	03-JUN-1998;	98US-0087827P.
PR	04-JUN-1998;	98US-0088025P.
PR	04-JUN-1998;	98US-0088028P.
PR	04-JUN-1998;	98US-0088029P.
PR	04-JUN-1998;	98US-0088033P.
PR	04-JUN-1998;	98US-0088326P.
PR	05-JUN-1998;	98US-0088167P.
PR	05-JUN-1998;	98US-0088202P.
PR	05-JUN-1998;	98US-0088212P.
PR	05-JUN-1998;	98US-0088217P.
PR	09-JUN-1998;	98US-0088655P.
PR	10-JUN-1998;	98US-0088722P.
PR	10-JUN-1998;	98US-0088738P.
PR	10-JUN-1998;	98US-0088740P.
PR	10-JUN-1998;	98US-0088811P.
PR	10-JUN-1998;	98US-0088824P.
PR	10-JUN-1998;	98US-0088825P.
PR	10-JUN-1998;	98US-0088826P.

PR	11-JUN-1998;	98US-0088861P.
PR	11-JUN-1998;	98US-0088863P.
PR	11-JUN-1998;	98US-0088876P.
PR	12-JUN-1998;	98US-0089090P.
PR	12-JUN-1998;	98US-0089105P.
PR	16-JUN-1998;	98US-0089512P.
PR	16-JUN-1998;	98US-0089514P.
PR	17-JUN-1998;	98US-0089538P.
PR	17-JUN-1998;	98US-0089598P.
PR	17-JUN-1998;	98US-0089653P.
PR	18-JUN-1998;	98US-0089908P.
PR	19-JUN-1998;	98US-0089952P.
PR	22-JUN-1998;	98US-0090246P.
PR	22-JUN-1998;	98US-0090252P.
PR	22-JUN-1998;	98US-0090254P.
PR	24-JUN-1998;	98US-0090429P.
PR	24-JUN-1998;	98US-0090435P.
PR	24-JUN-1998;	98US-0090444P.
PR	24-JUN-1998;	98US-0090461P.
PR	24-JUN-1998;	98US-0090535P.
PR	24-JUN-1998;	98US-0090540P.
PR	25-JUN-1998;	98US-0090676P.
PR	25-JUN-1998;	98US-0090678P.
PR	25-JUN-1998;	98US-0090688P.
PR	25-JUN-1998;	98US-0090690P.
PR	25-JUN-1998;	98US-0090694P.
PR	25-JUN-1998;	98US-0090695P.
PR	25-JUN-1998;	98US-0090696P.
PR	26-JUN-1998;	98US-00105413.
PR	26-JUN-1998;	98US-0090862P.
PR	26-JUN-1998;	98US-0090863P.
PR	26-JUN-1998;	98US-0091010P.
PR	01-JUL-1998;	98US-0091359P.
PR	01-JUL-1998;	98US-0091544P.
PR	02-JUL-1998;	98US-0091478P.
PR	02-JUL-1998;	98US-0091486P.
PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091632P.
PR	24-JUL-1998;	98US-0094006P.
PR	04-AUG-1998;	98US-0095282P.
PR	10-AUG-1998;	98US-0095998P.
PR	10-AUG-1998;	98US-0096012P.
PR	17-AUG-1998;	98US-0096757P.
PR	17-AUG-1998;	98US-0096766P.
PR	17-AUG-1998;	98US-0096867P.
PR	17-AUG-1998;	98US-0096891P.
PR	17-AUG-1998;	98US-0096897P.
PR	18-AUG-1998;	98US-0096949P.
PR	18-AUG-1998;	98US-0096959P.
PR	18-AUG-1998;	98US-0097022P.
PR	26-AUG-1998;	98US-0097952P.
PR	26-AUG-1998;	98US-0097954P.
PR	26-AUG-1998;	98US-0097955P.
PR	26-AUG-1998;	98US-0097971P.
PR	26-AUG-1998;	98US-0097974P.
PR	26-AUG-1998;	98US-0098014P.

PR	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098723P.
PR	02-SEP-1998;	98US-0098803P.
PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
PR	09-SEP-1998;	98US-0099602P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099812P.
PR	15-SEP-1998;	98US-0100388P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	16-SEP-1998;	98US-0101751P.
PR	16-SEP-1998;	98WO-US019330.
PR	17-SEP-1998;	98US-0100683P.
PR	17-SEP-1998;	98US-0100684P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101477P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101739P.
PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101922P.
PR	25-SEP-1998;	98US-0101786P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.

Query Match 98.9%; Score 1784.4; DB 7; Length 1879;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC	60
Db	94	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCACTGGCTCCTGCGCGCC	153
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	154	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	213
Qy	121	CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	214	CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	273

Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	274	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	334	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	393
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	394	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	453
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080

Db	1114	 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1234	 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1414	 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1534	 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1786
Db	1834	 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1879

RESULT 15

ACC86929

ID ACC86929 standard; cDNA; 1879 BP.

XX

AC ACC86929;

XX  
 DT 05-AUG-2003 (first entry)  
 XX  
 DE Human secreted polypeptide PRO852-encoding cDNA, SEQ ID NO:71.  
 XX  
 KW Human; PRO; secreted protein; transmembrane protein;  
 KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
 KW chondrocyte; proliferation; differentiation; cartilage disorder;  
 KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
 KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
 KW liver; drug screening; transgenic animal; genetic analysis;  
 KW antiarthritic; vulnerary; gene therapy; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003036159-A1.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 02-JUL-2002; 2002US-00188773.  
 XX  
 PR 18-SEP-1997; 97US-0059263P.  
 PR 18-SEP-1997; 97US-0059266P.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 21-OCT-1997; 97US-0063486P.  
 PR 24-OCT-1997; 97US-0063120P.  
 PR 24-OCT-1997; 97US-0063121P.  
 PR 28-OCT-1997; 97US-0063540P.  
 PR 28-OCT-1997; 97US-0063541P.  
 PR 28-OCT-1997; 97US-0063544P.  
 PR 28-OCT-1997; 97US-0063564P.  
 PR 29-OCT-1997; 97US-0063734P.  
 PR 31-OCT-1997; 97US-0063870P.  
 PR 31-OCT-1997; 97US-0064103P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 21-NOV-1997; 97US-0066120P.  
 PR 24-NOV-1997; 97US-0066466P.  
 PR 24-NOV-1997; 97US-0066772P.  
 PR 11-DEC-1997; 97US-0069335P.  
 PR 12-DEC-1997; 97US-0069425P.  
 PR 17-DEC-1997; 97US-0069870P.  
 PR 18-DEC-1997; 97US-0068017P.  
 PR 10-MAR-1998; 98US-0077450P.  
 PR 11-MAR-1998; 98US-0077632P.  
 PR 11-MAR-1998; 98US-0077649P.  
 PR 20-MAR-1998; 98US-0078886P.  
 PR 20-MAR-1998; 98US-0078939P.  
 PR 27-MAR-1998; 98US-0079664P.  
 PR 27-MAR-1998; 98US-0079786P.  
 PR 31-MAR-1998; 98US-0080107P.  
 PR 31-MAR-1998; 98US-0080194P.  
 PR 01-APR-1998; 98US-0080327P.  
 PR 01-APR-1998; 98US-0080333P.  
 PR 08-APR-1998; 98US-0081049P.  
 PR 08-APR-1998; 98US-0081070P.  
 PR 09-APR-1998; 98US-0081195P.  
 PR 15-APR-1998; 98US-0081838P.



PR	21-APR-1998;	98US-0082568P.
PR	21-APR-1998;	98US-0082569P.
PR	22-APR-1998;	98US-0082704P.
PR	22-APR-1998;	98US-0082797P.
PR	28-APR-1998;	98US-0083322P.
PR	29-APR-1998;	98US-0083495P.
PR	29-APR-1998;	98US-0083496P.
PR	29-APR-1998;	98US-0083499P.
PR	29-APR-1998;	98US-0083559P.
PR	05-MAY-1998;	98US-0084366P.
PR	06-MAY-1998;	98US-0084414P.
PR	07-MAY-1998;	98US-0084639P.
PR	07-MAY-1998;	98US-0084640P.
PR	07-MAY-1998;	98US-0084643P.
PR	15-MAY-1998;	98US-0085579P.
PR	15-MAY-1998;	98US-0085580P.
PR	15-MAY-1998;	98US-0085582P.
PR	15-MAY-1998;	98US-0085700P.
PR	18-MAY-1998;	98US-0086023P.
PR	22-MAY-1998;	98US-0086392P.
PR	22-MAY-1998;	98US-0086486P.
PR	28-MAY-1998;	98US-0087098P.
PR	28-MAY-1998;	98US-0087208P.
PR	02-JUN-1998;	98US-0087609P.
PR	02-JUN-1998;	98US-0087759P.
PR	03-JUN-1998;	98US-0087827P.
PR	04-JUN-1998;	98US-0088025P.
PR	04-JUN-1998;	98US-0088028P.
PR	04-JUN-1998;	98US-0088029P.
PR	04-JUN-1998;	98US-0088033P.
PR	04-JUN-1998;	98US-0088326P.
PR	05-JUN-1998;	98US-0088167P.
PR	05-JUN-1998;	98US-0088202P.
PR	05-JUN-1998;	98US-0088212P.
PR	05-JUN-1998;	98US-0088217P.
PR	09-JUN-1998;	98US-0088655P.
PR	10-JUN-1998;	98US-0088722P.
PR	10-JUN-1998;	98US-0088738P.
PR	10-JUN-1998;	98US-0088740P.
PR	10-JUN-1998;	98US-0088811P.
PR	10-JUN-1998;	98US-0088824P.
PR	10-JUN-1998;	98US-0088825P.
PR	10-JUN-1998;	98US-0088826P.
PR	11-JUN-1998;	98US-0088861P.
PR	11-JUN-1998;	98US-0088863P.
PR	11-JUN-1998;	98US-0088876P.
PR	12-JUN-1998;	98US-0089090P.
PR	12-JUN-1998;	98US-0089105P.
PR	16-JUN-1998;	98US-0089512P.
PR	16-JUN-1998;	98US-0089514P.
PR	17-JUN-1998;	98US-0089538P.
PR	17-JUN-1998;	98US-0089598P.
PR	17-JUN-1998;	98US-0089653P.
PR	18-JUN-1998;	98US-0089908P.
PR	19-JUN-1998;	98US-0089952P.
PR	22-JUN-1998;	98US-0090246P.
PR	22-JUN-1998;	98US-0090252P.

PR	22-JUN-1998;	98US-0090254P.
PR	24-JUN-1998;	98US-0090429P.
PR	24-JUN-1998;	98US-0090435P.
PR	24-JUN-1998;	98US-0090444P.
PR	24-JUN-1998;	98US-0090461P.
PR	24-JUN-1998;	98US-0090535P.
PR	24-JUN-1998;	98US-0090540P.
PR	25-JUN-1998;	98US-0090676P.
PR	25-JUN-1998;	98US-0090678P.
PR	25-JUN-1998;	98US-0090688P.
PR	25-JUN-1998;	98US-0090690P.
PR	25-JUN-1998;	98US-0090694P.
PR	25-JUN-1998;	98US-0090695P.
PR	25-JUN-1998;	98US-0090696P.
PR	26-JUN-1998;	98US-00105413.
PR	26-JUN-1998;	98US-0090862P.
PR	26-JUN-1998;	98US-0090863P.
PR	26-JUN-1998;	98US-0091010P.
PR	01-JUL-1998;	98US-0091359P.
PR	01-JUL-1998;	98US-0091544P.
PR	02-JUL-1998;	98US-0091478P.
PR	02-JUL-1998;	98US-0091486P.
PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091632P.
PR	24-JUL-1998;	98US-0094006P.
PR	04-AUG-1998;	98US-0095282P.
PR	10-AUG-1998;	98US-0095998P.
PR	10-AUG-1998;	98US-0096012P.
PR	17-AUG-1998;	98US-0096757P.
PR	17-AUG-1998;	98US-0096766P.
PR	17-AUG-1998;	98US-0096867P.
PR	17-AUG-1998;	98US-0096891P.
PR	17-AUG-1998;	98US-0096897P.
PR	18-AUG-1998;	98US-0096949P.
PR	18-AUG-1998;	98US-0096959P.
PR	18-AUG-1998;	98US-0097022P.
PR	26-AUG-1998;	98US-0097952P.
PR	26-AUG-1998;	98US-0097954P.
PR	26-AUG-1998;	98US-0097955P.
PR	26-AUG-1998;	98US-0097971P.
PR	26-AUG-1998;	98US-0097974P.
PR	26-AUG-1998;	98US-0098014P.
PR	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098723P.
PR	02-SEP-1998;	98US-0098803P.
PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
PR	09-SEP-1998;	98US-0099602P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099812P.
PR	15-SEP-1998;	98US-0100388P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	16-SEP-1998;	98US-0101751P.



Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
		*	
Db	514	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353

Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTCTTTTGATTCTTGATTTTCAAGCTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCAGTCTTTTGATTCTTGATTTTCAAGCTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1879

Search completed: February 28, 2004, 05:52:16  
 Job time : 723 secs

OM nucleic - nucleic search, using sw model

Run on: February 28, 2004, 03:40:07 ; Search time 156 Seconds  
 (without alignments)  
 6417.509 Million cell updates/sec

Title: US-09-668-314C-1  
 Perfect score: 1804  
 Sequence: 1 atgggcgcactggcccgggc.....aaaccaaaaaaaaaaaaaaa 1804

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1804	100.0	1804	4	US-09-548-372D-1	Sequence 1, Appli
2	1804	100.0	1804	4	US-09-548-367D-1	Sequence 1, Appli
3	1804	100.0	1804	4	US-09-551-853D-1	Sequence 1, Appli
4	1768.2	98.0	1873	4	US-09-215-450-18	Sequence 18, Appl
5	1765.6	97.9	1862	3	US-08-999-723-1	Sequence 1, Appli
6	1765.6	97.9	1862	3	US-09-434-427-1	Sequence 1, Appli
7	1478.6	82.0	2429	4	US-09-215-450-1	Sequence 1, Appli
8	1134.2	62.9	1545	3	US-09-717-432-1	Sequence 1, Appli
9	1134.2	62.9	1545	4	US-09-912-484-1	Sequence 1, Appli
10	1104.6	61.2	2514	4	US-09-280-116-32	Sequence 32, Appl
11	953.6	52.9	1021	4	US-09-280-116-85	Sequence 85, Appl

12	397.4	22.0	2348	4	US-09-724-566A-42	Sequence 42, Appl
13	397.4	22.0	2348	4	US-09-724-566A-44	Sequence 44, Appl
14	397.4	22.0	16080	4	US-09-724-566A-48	Sequence 48, Appl
15	395	21.9	1503	4	US-09-724-566A-1	Sequence 1, Appli
16	395	21.9	2070	4	US-09-548-372D-3	Sequence 3, Appli
17	395	21.9	2070	4	US-09-548-367D-3	Sequence 3, Appli
18	395	21.9	2070	4	US-09-551-853D-3	Sequence 3, Appli
19	395	21.9	3252	4	US-09-604-608-1	Sequence 1, Appli
20	393.4	21.8	2541	4	US-09-009-191-1	Sequence 1, Appli
21	387.2	21.5	2370	4	US-09-009-191-3	Sequence 3, Appli
22	386	21.4	1380	4	US-09-548-372D-23	Sequence 23, Appl
23	386	21.4	1380	4	US-09-548-367D-23	Sequence 23, Appl
24	386	21.4	1380	4	US-09-551-853D-23	Sequence 23, Appl
25	385	21.3	1362	4	US-09-548-372D-29	Sequence 29, Appl
26	385	21.3	1362	4	US-09-548-367D-29	Sequence 29, Appl
27	385	21.3	1362	4	US-09-551-853D-29	Sequence 29, Appl
28	385	21.3	1380	4	US-09-548-372D-31	Sequence 31, Appl
29	385	21.3	1380	4	US-09-548-367D-31	Sequence 31, Appl
30	385	21.3	1380	4	US-09-551-853D-31	Sequence 31, Appl
31	384.6	21.3	1341	4	US-09-548-372D-21	Sequence 21, Appl
32	384.6	21.3	1341	4	US-09-548-367D-21	Sequence 21, Appl
33	384.6	21.3	1341	4	US-09-551-853D-21	Sequence 21, Appl
34	382.4	21.2	1302	4	US-09-548-372D-25	Sequence 25, Appl
35	382.4	21.2	1302	4	US-09-548-367D-25	Sequence 25, Appl
36	382.4	21.2	1302	4	US-09-551-853D-25	Sequence 25, Appl
37	381	21.1	1506	4	US-09-713-158-1	Sequence 1, Appli
38	381	21.1	2043	4	US-09-548-372D-7	Sequence 7, Appli
39	381	21.1	2043	4	US-09-548-367D-7	Sequence 7, Appli
40	381	21.1	2043	4	US-09-551-853D-7	Sequence 7, Appli
41	380.8	21.1	1278	4	US-09-548-372D-27	Sequence 27, Appl
42	380.8	21.1	1278	4	US-09-548-367D-27	Sequence 27, Appl
43	380.8	21.1	1278	4	US-09-551-853D-27	Sequence 27, Appl
44	294	16.3	306	4	US-09-280-116-52	Sequence 52, Appl
45	291.2	16.1	1977	4	US-09-548-372D-5	Sequence 5, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-548-372D-1

; Sequence 1, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23



; PRIOR APPLICATION NUMBER: US 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1804  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-548-372D-1

Query Match 100.0%; Score 1804; DB 4; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy    121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy    361 ACCCCGCACTCCTACATAGACACGTA CTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCCCGCACTCCTACATAGACACGTA CTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy    541 TTTGAATCAGAGAATTTCTTTTTCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TTTGAATCAGAGAATTTCTTTTTCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600

Qy    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
```

Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGTCAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGTCAGCGTCGCCCC	1500

```

Qy      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
          |||
Db      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560

Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
          |||
Db      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620

Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1680
          |||
Db      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1680

Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          |||
Db      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
          |||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800

Qy      1801 AAAA 1804
          |||
Db      1801 AAAA 1804

```

## RESULT 2

US-09-548-367D-1

; Sequence 1, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1804

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-548-367D-1

```

Query Match          100.0%;  Score 1804;  DB 4;  Length 1804;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 1804;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTA TTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTA TTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900

Db	841	 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	 CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Db	1141	 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740

```

Db      1681 GCTCCCAGATGCCTTCTAGATTCACGTGCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAAAAA 1800
          |||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAAAAA 1800
Qy      1801 AAAA 1804
          |||
Db      1801 AAAA 1804

```

# RESULT 3

US-09-551-853D-1

```

; Sequence 1, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-551-853D-1

```

```

Query Match      100.0%; Score 1804; DB 4; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCAGTGGCTCCTGCGCGCC 60
          |||
Db      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCAGTGGCTCCTGCGCGCC 60
Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
          |||
Db      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
Qy      121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
          |||
Db      121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
          |||

```



Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080



Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

RESULT 4

US-09-215-450-18

; Sequence 18, Application US/09215450

; Patent No. 6635748  
; GENERAL INFORMATION:  
; APPLICANT: Giese, Klaus  
; APPLICANT: Xin, Hong  
; TITLE OF INVENTION: METASTATIC BREAST AND COLON CANCER REGULATED GENES  
; FILE REFERENCE: 1451.100 / 210030.447  
; CURRENT APPLICATION NUMBER: US/09/215,450  
; CURRENT FILING DATE: 1998-12-17  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 18  
; LENGTH: 1873  
; TYPE: DNA  
; ORGANISM: human  
US-09-215-450-18

Query Match 98.0%; Score 1768.2; DB 4; Length 1873;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1770; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	101	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	160
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	161	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC	220
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	221	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	280
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	281	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	340
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	341	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	400
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	401	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	460
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	461	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	520
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	521	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	580
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	581	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	640
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600

Db	641	TTTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	700
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	701	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	760
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	761	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	820
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	821	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	880
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	881	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	940
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	941	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	1000
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	1001	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1060
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1061	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1120
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1121	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1180
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1181	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1240
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Db	1241	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1300
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1301	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1360
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1361	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1420
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1421	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1480
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440

```

Db      1481 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1540
Qy      1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC 1500
          |||
Db      1541 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC 1600
Qy      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
          |||
Db      1601 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1660
Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
          |||
Db      1661 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1720
Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1680
          |||
Db      1721 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1780
Qy      1681 GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          |||
Db      1781 GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1840
Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAA 1773
          |||
Db      1841 CTCCCTACTTCCAAGAAAAAAAATAATTAAAAAAA 1873

```

# RESULT 5

US-08-999-723-1

```

; Sequence 1, Application US/08999723A
; Patent No. 6025180
; GENERAL INFORMATION:
; APPLICANT: Powell, David J.
; APPLICANT: Southan, Christopher
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Evans, Joanne R.
; TITLE OF INVENTION: ASP1
; FILE REFERENCE: GH70262
; CURRENT APPLICATION NUMBER: US/08/999,723A
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1862
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-999-723-1

```

```

Query Match          97.9%;  Score 1765.6;  DB 3;  Length 1862;
Best Local Similarity 99.8%;  Pred. No. 0;
Matches 1768;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;

```

```

Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
          |||
Db      91 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 150
Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC 120

```

Db	151	 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAAC	210
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	211	 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	270
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	271	 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	330
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	331	 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	390
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	391	 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	450
Qy	361	ACCCCGCACTCCTACATAGACACGTA TTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	451	 ACCCCGCACTCCTACATAGACACGTA TTTGACACAGAGAGGTCTAGCACATAACCGCTCC	510
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	511	 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	570
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	571	 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	630
Qy	541	TTTGAATCAGAGAATTTCTTTTTCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	631	 TTTGAATCAGAGAATTTCTTTTTCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	690
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	691	 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	750
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	751	 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	810
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	811	 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	870
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	871	 GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	930
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	931	 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	990
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960

Db	991	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1050
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1051	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1110
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1111	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1170
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1171	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1230
Qy	1141	ATTCAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1231	ATTCAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1290
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1291	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1350
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1351	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1410
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1411	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1470
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1471	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1530
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1531	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1590
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1591	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1650
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1651	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1710
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1711	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1770
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1771	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1830
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAATAAAAAA	1772
Db	1831	CTCCCTACTTCCAAGAAAAATAATTAATAAAAAA	1862

RESULT 6

US-09-434-427-1

; Sequence 1, Application US/09434427  
 ; Patent No. 6162630  
 ; GENERAL INFORMATION:  
 ; APPLICANT: POWELL, DAVID J.  
 ; APPLICANT: SOUTHAN, CHRISTOPHER  
 ; APPLICANT: CHAPMAN, CONRAD G.  
 ; APPLICANT: EVANS, JOANNE R.  
 ; TITLE OF INVENTION: ASP1  
 ; FILE REFERENCE: GH-70262-D1  
 ; CURRENT APPLICATION NUMBER: US/09/434,427  
 ; CURRENT FILING DATE: 1999-11-04  
 ; EARLIER APPLICATION NUMBER: US 08/999,723  
 ; EARLIER FILING DATE: 1997-10-06  
 ; EARLIER APPLICATION NUMBER: UK 9626022.9  
 ; EARLIER FILING DATE: 1996-12-14  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1862  
 ; TYPE: DNA  
 ; ORGANISM: HOMO SAPIENS  
 US-09-434-427-1

Query Match 97.9%; Score 1765.6; DB 3; Length 1862;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1768; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	91	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	150
Qy	61	GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	151	GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	210
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	211	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	270
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCCATG	240
Db	271	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGCCCATG	330
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	331	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	390
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	391	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	450
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420



Db	451	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	510
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	511	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	570
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	571	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	630
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	631	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	690
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	691	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	750
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	751	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	810
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	811	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	870
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	871	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	930
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	931	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	990
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	991	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1050
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1051	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1110
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1111	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1170
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1171	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1230
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGGCATTTCCCCA	1200
Db	1231	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCCGGCATTTCCCCA	1290
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1291	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1350

```

Qy      1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
          |||
Db      1351 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1410

Qy      1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT 1380
          |||
Db      1411 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT 1470

Qy      1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA 1440
          |||
Db      1471 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTTATGCGCTCATGAGCGTCTGTGGA 1530

Qy      1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC 1500
          |||
Db      1531 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC 1590

Qy      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
          |||
Db      1591 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1650

Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
          |||
Db      1651 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1710

Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1680
          |||
Db      1711 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1770

Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
          |||
Db      1771 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1830

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAATAAAAA 1772
          |||
Db      1831 CTCCCTACTTCCAAGAAAAATAATTAATAAAAA 1862

```

RESULT 7

US-09-215-450-1

; Sequence 1, Application US/09215450

; Patent No. 6635748

; GENERAL INFORMATION:

; APPLICANT: Giese, Klaus

; APPLICANT: Xin, Hong

; TITLE OF INVENTION: METASTATIC BREAST AND COLON CANCER REGULATED GENES

; FILE REFERENCE: 1451.100 / 210030.447

; CURRENT APPLICATION NUMBER: US/09/215,450

; CURRENT FILING DATE: 1998-12-17

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 2429

; TYPE: DNA

; ORGANISM: human

US-09-215-450-1

Query Match 82.0%; Score 1478.6; DB 4; Length 2429;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1484; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy	305	CGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGAACCC	364
Db	213	CTCACCAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGCAGGAAACCC	272
Qy	365	CGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGG	424
Db	273	CGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGG	332
Qy	425	GCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACC	484
Db	333	GCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACC	392
Qy	485	TCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTGTG	544
Db	393	TCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATTTTGTG	452
Qy	545	AATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTATG	604
Db	453	AATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTATG	512
Qy	605	CCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAAG	664
Db	513	CCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAAG	572
Qy	665	CAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGAT	724
Db	573	CAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGAT	632
Qy	725	CTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAG	784
Db	633	CTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAG	692
Qy	785	ACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGG	844
Db	693	ACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGG	752
Qy	845	AAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCG	904
Db	753	AAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCG	812
Qy	905	TGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGAAG	964
Db	813	TGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGAAG	872
Qy	965	CTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGC	1024
Db	873	CTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGC	932
Qy	1025	TGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACC	1084
Db	933	TGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACC	992
Qy	1085	TGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTC	1144

Db	993		TGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTC	1052
Qy	1145		AGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCATCCCA	1204
Db	1053		AGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCATCCCA	1112
Qy	1205		CAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAG	1264
Db	1113		CAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAG	1172
Qy	1265		CCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGT	1324
Db	1173		CCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGT	1232
Qy	1325		CTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGT	1384
Db	1233		CTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGT	1292
Qy	1385		CTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCA	1444
Db	1293		CTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCA	1352
Qy	1445		TCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTG	1504
Db	1353		TCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTG	1412
Qy	1505		ACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCA	1564
Db	1413		ACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCA	1472
Qy	1565		GGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCA	1624
Db	1473		GGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCA	1532
Qy	1625		GCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCTGCTC	1684
Db	1533		GCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCTGCTC	1592
Qy	1685		CCAGATGCCTTCTAGATTCAGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCC	1744
Db	1593		CCAGATGCCTTCTAGATTCAGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCC	1652
Qy	1745		CTACTTCCAAGAAAAATAATTAATAAAAAAAAAACTTCATTCTAAACCAAAAAAA	1797
Db	1653		CTACTTCCAAGAAAAATAATTAATAAAAAAAAAACTTCATTCTAAACCAAAACAGA	1705

RESULT 8

US-09-717-432-1

; Sequence 1, Application US/09717432

; Patent No. 6291223

; GENERAL INFORMATION:

; APPLICANT: ZHU, YUAN

; APPLICANT: LI, XIAOTONG

; APPLICANT: CHRISTIE, GARY

; APPLICANT: POWELL, DAVID J.

; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (mASP1)  
; FILE REFERENCE: GP-70663  
; CURRENT APPLICATION NUMBER: US/09/717,432  
; CURRENT FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: 60/166,974  
; PRIOR FILING DATE: 1999-11-23  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1545  
; TYPE: DNA  
; ORGANISM: MUS MUSCULUS  
US-09-717-432-1

Query Match 62.9%; Score 1134.2; DB 3; Length 1545;  
Best Local Similarity 83.6%; Pred. No. 5.5e-260;  
Matches 1302; Conservative 0; Mismatches 243; Indels 12; Gaps 1;

```
Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
        ||||| ||| || || || |||| | ||||| ||||| || | ||
Db      1 ATGGGCGCGCTGCTTCGAGCACTCTTGCTCCTGGTGCTGGCGCAGTGGCTCTTGAGTGCG 60

Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
        | ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 GTCCCCGCGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCAAGTGGCCGGGGCCACGAAC 120

Qy    121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
        | | || || | || |||| ||||| || | || || |||| || ||
Db    121 CACAGAGCCTCGGCTGTTCCCGGACTCGGGACCCCGAGTTGCCCCGGGCCGATGGTCTG 180

Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACCTTCTTGGCCATG 240
        || |||| ||||| || | || | ||||| ||||| |||
Db    181 GCCCTCGCACTGGAGCCTGTCAGGGC-----TACTGCCAACTTCTTGGCTATG 228

Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    229 GTGGACAACCTTCAGGGGGACTCTGGCCGCGGCTACTACCTAGAGATGCTGATCGGGACC 288

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
        || ||||| ||||| || ||||| ||||| ||||| || ||||| ||
Db    289 CCTCCGCAGAAGGTACAGATTCTTGTGGACACTGGAAGCAGTAACTTCGCTGTGGCAGGT 348

Qy    361 ACCCCGCACTCCTACATAGACACGTA CTTTGACACAGAGAGGTCTAGCACATAACCGCTCC 420
        |||| ||||| ||||| ||||| ||||| || ||||| ||||| |||||
Db    349 GCCCCACACTCCTACATAGACACCTACTTTGACTCAGAGAGCTCCAGCACATAACCACTCC 408

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db    409 AAGGGCTTTGATGTCACTGTGAAGTACACACAGGGAAGCTGGACTGGCTTTGTTGGTGAG 468

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT 540
        |||| ||||| ||||| ||||| || |||| | ||||| ||||| |||||
Db    469 GACCTTGTACCATCCCCAAAGGCTTCAACAGCTCTTCTTGGTCAATATTGCCACTATT 528

Qy    541 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
        || || || ||||| ||||| ||||| ||||| ||||| ||||| || |||
Db    529 TTCGAGTCTGAGAATTTCTTTTGCCTGGTATTAAATGGAATGGAATCCTTGGACTTGCT 588
```

Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	589	TATGCTGCTTTGGCCAAGCCATCAAGCTCTCTGGAGACATTTTTTTGATTCCCTGGTGGCC	648
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	649	CAAGCAAAGATTCCAGACATTTTCTCCATGCAGATGTGCGGGGCTGGATTGCCAGTAGCT	708
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	709	GGTTCTGGTACCAACGGAGGTAGTCTTGTCTTGGGTGGGATTGAACCAAGTTTGTATAAA	768
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	769	GGAGATATCTGGTATAACCCCAATTAAAGAGGAATGGTACTATCAAATAGAAATCCTGAAG	828
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	829	TTGGAAATTGGAGGCCAGAACCTCAACCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	888
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	889	ATTGTGGACAGTGGCACCACGCTCCTGCGCCTGCCCCAGAAGGTGTTTGATGCAGTGGTG	948
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	949	GAAGCTGTGGCACGAACATCTCTGATTCCAGAGTTTTCTGATGGCTTCTGGACAGGGGCC	1008
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1009	CAGCTGGCATGCTGGACAAATTCTGAAACGCCATGGGCATATTTCCCTAAGATTTCTATC	1068
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1069	TACCTGAGAGATGAGAATGCCAGTCGCTCCTTCCGGATCACCATTCTCCACAGCTCTAC	1128
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1129	ATTCAGCCCATGATGGGAGCTGGTTTCAATTATGAATGCTACCGTTTTGGTATCTCCTCT	1188
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1189	TCCACAAATGCGCTGGTGATTGGTGCGACCGTGATGGAAGGCTTCTACGTGGTCTTTGAC	1248
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1249	AGAGCTCAGAGGAGGGTGGGCTTTGCAGTGAGTCCCTGTGCAGAGATTGAAGGTACCACA	1308
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1309	GTGTCTGAAATTTCTGGGCCCTTTTCCACGGAAGACATAGCCAGCAACTGTGTTCAGCA	1368
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1369	CAGGCTCTGAATGAGCCCATCTTGTGGATTGTGTCCTATGCCCTGATGAGTGTGTGTGGA	1428

```

Qy      1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGTCAGCGTCGCCCC 1500
          ||||| ||||| || | ||| |||| | ||||| ||| | | || | | |||
Db      1429 GCCATTCTCCTGGTTCTGATCCTCCTCCTGCTGCTCCCGCTGCACTGCCGTCATGCCCCC 1488

Qy      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGA 1557
          || ||||| ||||| || || ||||| ||||| || ||||| ||||| |||||
Db      1489 CGAGACCCTGAGGTAGTTAACGATGAGTCCTCACTAGTCAGACATCGCTGGAAATGA 1545

```

RESULT 9

US-09-912-484-1

```

; Sequence 1, Application US/09912484
; Patent No. 6358725
; GENERAL INFORMATION:
; APPLICANT: Christie, Gary
; APPLICANT: Li, Xiaotong
; APPLICANT: Powell, David J.
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (mASP1)
; FILE REFERENCE: GP-70663-D1
; CURRENT APPLICATION NUMBER: US/09/912,484
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/166,974
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/717,432
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1545
; TYPE: DNA
; ORGANISM: MUS MUSCULUS
US-09-912-484-1

```

```

Query Match          62.9%; Score 1134.2; DB 4; Length 1545;
Best Local Similarity 83.6%; Pred. No. 5.5e-260;
Matches 1302; Conservative 0; Mismatches 243; Indels 12; Gaps 1;

```

```

Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
          ||||| ||||| || || || || |||| | ||||| ||||| || || ||
Db      1 ATGGGCGCGCTGCTTCGAGCACTCTTGCTCCTGGTGCTGGCGCAGTGGCTCCTGAGTGCG 60

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
          | ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 GTCCCCGCGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCAAGTGGCCGGGGCCACGAAC 120

Qy      121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
          | | || || | || |||| ||||| || || || |||| | || ||
Db      121 CACAGAGCCTCGGCTGTTCCCGGACTCGGGACCCCGAGTTGCCCCGGGCGGATGGTCTG 180

Qy      181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
          || ||||| ||||| || || || || ||||| ||||| ||||| |||||
Db      181 GCCCTCGCACTGGAGCCTGTCAGGGC-----TACTGCCAACTTCTTGGCTATG 228

Qy      241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      229 GTGGACAACCTTCAGGGGGACTCTGGCCGCGGCTACTACCTAGAGATGCTGATCGGGACC 288

```



Qy	301	CCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	289	CCTCCGCAGAAGGTACAGATTCTTGTGGACACTGGAAGCAGTAACTTCGCTGTGGCAGGT	348
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	349	GCCCCACACTCCTACATAGACACCTACTTTGACTCAGAGAGCTCCAGCACATAACCACTCC	408
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	409	AAGGGCTTTGATGTCACGTGTGAAGTACACACAGGGAAGCTGGACTGGCTTTGTTGGTGAG	468
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	469	GACCTTGTACCATCCCCAAAGGCTTCAACAGCTCTTTCTTGGTCAATATTGCCACTATT	528
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	529	TTCGAGTCTGAGAATTTCTTTTTGCCTGGTATTAAATGGAATGGAATCCTTGGACTTGCT	588
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	589	TATGCTGCTTTGGCCAAGCCATCAAGCTCTCTGGAGACATTTTTTGATTCCCTGGTGGCC	648
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	649	CAAGCAAAGATTCCAGACATTTTCTCCATGCAGATGTGCGGGGCTGGATTGCCAGTAGCT	708
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	709	GGTTCTGGTACCAACGGAGGTAGTCTTGTCTTGGGTGGGATTGAACCAAGTTTGTATAAA	768
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	769	GGAGATATCTGGTATAACCCCAATTAAAGAGGAATGGTACTATCAAATAGAAATCCTGAAG	828
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	829	TTGGAAATTGGAGGCCAGAACCTCAACCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	888
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	889	ATTGTGGACAGTGGCACCACGCTCCTGCGCCTGCCCCAGAAGGTGTTTGATGCAGTGGTG	948
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	949	GAAGCTGTGGCACGAACATCTCTGATTCCAGAGTTTTCTGATGGCTTCTGGACAGGGGCC	1008
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1009	CAGCTGGCATGCTGGACAAATTCTGAAACGCCATGGGCATATTTCCCTAAGATTTCTATC	1068
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1069	TACCTGAGAGATGAGAATGCCAGTCGCTCCTTCCGGATCACCATTCTCCACAGCTCTAC	1128

Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1129	ATTCAGCCCATGATGGGAGCTGGTTTCAATTATGAATGCTACCGTTTTGGTATCTCCTCT	1188
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1189	TCCACAAATGCGCTGGTGATTGGTGCGACCGTGATGGAAGGCTTCTACGTGGTCTTTGAC	1248
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1249	AGAGCTCAGAGGAGGGTGGGCTTTGCAGTGAGTCCCTGTGCAGAGATTGAAGGTACCACA	1308
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1309	GTGTCTGAAATTTCTGGGCCCTTTTCCACGGAAGACATAGCCAGCAACTGTGTTCCAGCA	1368
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1369	CAGGCTCTGAATGAGCCCATCTTGTGGATTGTGTCCTATGCCCTGATGAGTGTGTGTGGA	1428
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1429	GCCATTCTCCTGGTTCTGATCCTCCTCCTGCTGCTCCCGCTGCACTGCCGTCATGCCCC	1488
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGA	1557
Db	1489	CGAGACCCTGAGGTAGTTAACGATGAGTCCTCACTAGTCAGACATCGCTGGAAATGA	1545

```
Query Match      61.2%;   Score 1104.6;   DB 4;   Length 2514;  
Best Local Similarity 92.9%;   Pred. No. 7.1e-253;  
Matches 1428; Conservative    0; Mismatches    64; Indels    45; Gaps    24;
```

.

```
Qy          305 CGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGAACCC 364  
              | ||| |  
Db           213 CTCACCAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGG-AGGAACCC 271
```

Qy	365	CGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGG	424
Db	272	CGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGG	331
Qy	425	GCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACC	484
Db	332	GCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACC	391
Qy	485	TCGTCACCATCCCCAAAGGCTTC-AATACTTCTTTTCTTGTC AACATTGCCACTATTTTT	543
Db	392	TCGTCACCATCCCCAAAGGCTTCAAATACTTCTTTTCTTGTC AACATTGCCACTATTTTT	451
Qy	544	GAATCAGA-GAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTA	602
Db	452	GAATCAGAGGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCTTA	511
Qy	603	TGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTG---AC	659
Db	512	TGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGAACAC	571
Qy	660	ACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCC-GGCTTGCCCGTTG	718
Db	572	AAGCAAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGGCTTGCCCGTTG	631
Qy	719	CTGG-----ATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTT	773
Db	632	GCTGGGATTCTGGGGAACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTT	691
Qy	774	GTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAAT	833
Db	692	GTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAAT	751
Qy	834	TCTGAAATT---GGAAATTGGAGGCCAAAGCCTTAAT-----CTGGACTGCAGAGAGTA	884
Db	752	TCTTGAAATTGGGAAATTGGGAGGCCAAAGCTTTAATTCTTGGGACTGCAGGAGGAGTAT	811
Qy	885	TAACGCAGACAAGG--CCATCGTGGACAGT-GGCACCACGCTGCTGCGCCT--GCCCCAG	939
Db	812	TAACGCAGACAAGGGCCATCGTTGGACAGTGGGCACCACGCTGCTGCGCCTTGCCCCCAG	871
Qy	940	AAGGTGTTTGATGCGGTGGT-GGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTC	998
Db	872	AAGGTGTTTGATGCGGTGGTGGGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTC	931
Qy	999	TGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTC	1058
Db	932	TGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTC	991
Qy	1059	TTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTAT	1118
Db	992	TTACTTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTAT	1051
Qy	1119	CACAATCCTGCCTCAGCTTTACATTAGCCCATGATGGGGGCCGGCCTGAATTATGAATG	1178
Db	1052	CACAATCCTGCCTCAGCTTTACATTAGCCCATGATGGGGGCCGGCCTGAATTATGAATG	1111
Qy	1179	TTACCGATTGCGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGA	1238

```

      |||
Db      1112 TTACCGATTCTGGCATTTCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGA 1171
      |||
Qy      1239 GGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTG 1298
      |||
Db      1172 GGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTG 1231
      |||
Qy      1299 TGCAGAAATTGCA-GGTGCTGC-AGTGTCTGAAATTTCCGGGCCTTTCTC-AACAGAGGA 1355
      |||
Db      1232 TGCAGAAATTGCACGGTGCTGCAAGTGTCTGAAATTTCCGGGCCTTTCTCAAACAGAGGA 1291
      |||
Qy      1356 TGTAGCCAG-CAACTGTGTCCCGCTC-AGTCTTTGAGCGA-GCCCATTTTGTGGATTGT 1412
      |||
Db      1292 TGTAGCCAGCCAACTGTGTCCCGCTCAAGTCTTTGAGCGACGCCCATTTTGTGGATTGT 1351
      |||
Qy      1413 GTCC----TATGCGCTCATGAGCGTCTGTGG-AGCCATCCTCCTTGTC-TTAATCGTCCT 1466
      |||
Db      1352 GTCCCTATGCCGCTCAATGAAGCGTCTGTGGAAGCCATCCTCCTTGTCGTTAATTTCAGTC 1411
      |||
Qy      1467 GCTGCTGC----TGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATG 1522
      |||
Db      1412 GCTGCTGCTGCTTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATG 1471
      |||
Qy      1523 ATGAGTCCTCTCT-GGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA 1581
      |||
Db      1472 ATGAGTCCTCTCTGGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA 1531
      |||
Qy      1582 CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGG 1641
      |||
Db      1532 CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGG 1591
      |||
Qy      1642 CGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGAT 1701
      |||
Db      1592 CGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGAT 1651
      |||
Qy      1702 TCACTGTCTTTTGATTCTTGATTTTCAAGC-TTTCAAATCCTCCCTACTTCCAAGAAAAA 1760
      |||
Db      1652 TCACTGTCTTTTGATTCTTGATTTTCAAGCTTTTCAAATCCTCCCTACTTCCAAGAAAAA 1711
      |||
Qy      1761 TAATTAAAAAAAACCTTCATTCTAAACCAAAAAAA 1797
      |||
Db      1712 TAATTAAAAAAAACCTTCATTCTAAACCAAAACAGA 1748

```

RESULT 11

US-09-280-116-85

; Sequence 85, Application US/09280116A

; Patent No. 6331427

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs

; FILE REFERENCE: 5800-24, 035800/176965

; CURRENT APPLICATION NUMBER: US/09/280,116A

; CURRENT FILING DATE: 1999-03-26

; NUMBER OF SEQ ID NOS: 268

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 85

```
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: aspartyl proteases
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1021)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-85
```

```
Query Match          52.9%;  Score 953.6;  DB 4;  Length 1021;
Best Local Similarity 98.8%;  Pred. No. 3.7e-217;
Matches 971;  Conservative 0;  Mismatches 10;  Indels 2;  Gaps 1;
```

```
Qy      98 TCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTG 157
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38 TCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGAGCCCTG 97

Qy     158 CCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG 217
        |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      98 CCGAGCGCCACGCCGACGGCTNNGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG 157

Qy     218 GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACT 277
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     158 GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACT 217

Qy     278 ACCTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAA 337
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     218 ACCTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAA 277

Qy     338 GCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAG 397
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     278 GCAGTAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAG 337

Qy     398 AGAGGTCTAGCACATAACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAA 457
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     338 AGAGGTCTAGCACATAACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAA 397

Qy     458 GCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTT 517
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     398 GCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTT 457

Qy     518 TTCTTGTC AACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAAT 577
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     458 TTCTTGTC AACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAAT 517

Qy     578 GGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGA 637
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     518 GGAATGGAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGA 577

Qy     638 CCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGT 697
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     578 CCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGT 637

Qy     698 GTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTG 757
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db 638 GTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTG 697  
 Qy 758 GAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGT 817  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 698 GAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGT 757  
 Qy 818 ACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCA 877  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 758 ACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCA 817  
 Qy 878 GAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCC 937  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 818 GAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCC 877  
 Qy 938 AGAAGGTGTTTGATGC--GGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATT 995  
 |||||||||||||||| | | | ||||||||||||||||||||||||||||||||||||  
 Db 878 AGAAGGTGTTTGATGCCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATT 937  
 Qy 996 CTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTG 1055  
 |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||  
 Db 938 CTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTG 997  
 Qy 1056 GTCTTACTTCCCTAAAATCTCCA 1078  
 |||||||||||||||||||| ||  
 Db 998 GTCTTACTTCCCTAAAATCTTCA 1020

RESULT 12

US-09-724-566A-42

; Sequence 42, Application US/09724566A

; Patent No. 6627739

; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.

; APPLICANT: Basi, Guriqbal

; APPLICANT: Doane, Minh Tam

; APPLICANT: Frigon, No. 6627739mand

; APPLICANT: John, Varghese

; APPLICANT: Power, Michael

; APPLICANT: Sinha, Sukanto

; APPLICANT: Tatsuno, Gwen

; APPLICANT: Tung, Jay

; APPLICANT: Wang, Shuwen

; APPLICANT: McConlogue, Lisa

; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and

; TITLE OF INVENTION: Methods

; FILE REFERENCE: 228-US-NEWC2

; CURRENT APPLICATION NUMBER: US/09/724,566A

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 09/501,708

; PRIOR FILING DATE: 2000-02-10

; PRIOR APPLICATION NUMBER: 60/119,571

; PRIOR FILING DATE: 1999-02-10

; PRIOR APPLICATION NUMBER: 60/139,172

; PRIOR FILING DATE: 1999-06-15

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 42

; LENGTH: 2348  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-566A-42

Query Match 22.0%; Score 397.4; DB 4; Length 2348;  
Best Local Similarity 55.0%; Pred. No. 7.1e-85;  
Matches 863; Conservative 0; Mismatches 676; Indels 30; Gaps 3;

```
Qy      2 TGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCCG 61
      |||| ||| ||| ||| | ||| ||| ||||| || || | |
Db    238 TGGGGGCGAGGCGCCAGGGACGGACGTGGGCCAGTGCGAGCCCAGAGGGCCCGAAGGCCGG 297

Qy     62 CCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAACC 121
      || ||||| || | | ||| | || || ||||| || |
Db    298 GGCCCACCATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGC 357

Qy    122 GCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTGG 181
      | | || | || | || || || || | | |||
Db    358 CTGCCACGGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCC 417

Qy    182 CGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGC----- 224
      | || | ||| || ||| || | || || | |||
Db    418 CCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGG 477

Qy    225 -CAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGG 283
      || ||| ||| ||||| ||||| ||| | || || | ||||| |||
Db    478 GCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGG 537

Qy    284 AGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTA 343
      ||||| | || | ||||| ||| | || || || || || |||||
Db    538 AGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTA 597

Qy    344 ACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT 403
      ||||| |||| | ||| ||| ||| | | ||| || | || ||
Db    598 ACTTTGCAGTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGT 657

Qy    404 CTAGCACATAACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGA 463
      | ||||| |||| | | | ||| ||| |||| || || | |||
Db    658 CCAGCACATAACGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGG 717

Qy    464 CGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTG 523
      || | || |||| || | ||||| || ||| ||| || | ||
Db    718 AAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTG 777

Qy    524 TCAACATTGCCACTATTTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATG 583
      ||||| || | ||||| || ||||| | || || ||| |
Db    778 CCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAG 837

Qy    584 GAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCT 643
      | || || || || || |||| ||||| ||| || ||||| || |||
Db    838 GCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTCT 897

Qy    644 TCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAG 703
      | ||||| |||| | || | ||| ||||| ||||| ||||| |
Db    898 TTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTG 957
```



Qy	704	CCGGCTTGCCCGT-----TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGG	754
Db	958	CTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTG	1017
Qy	755	GTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGT	814
Db	1018	GAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGT	1077
Qy	815	GGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACT	874
Db	1078	GGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACT	1137
Qy	875	GCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGC	934
Db	1138	GCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGC	1197
Qy	935	CCCAGAAGGTGTTTGATGCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAAT	994
Db	1198	CCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGT	1257
Qy	995	TCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTT	1054
Db	1258	TCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTT	1317
Qy	1055	GGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCC	1114
Db	1318	GGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCC	1377
Qy	1115	GTATCACAATCCTGCCTCAGCTTTACATTACAGCCCATGATGGGGGCCGGCCTG---AATT	1171
Db	1378	GCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAG	1437
Qy	1172	ATGAATGTTACCGATTTCGGCATTTCCCATCCACAAATGCGCTGGTGATCGGTGCCACGG	1231
Db	1438	ACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTA	1497
Qy	1232	TGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGA	1291
Db	1498	TCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCA	1557
Qy	1292	GCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAG	1351
Db	1558	GCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCT	1617
Qy	1352	AGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTG	1411
Db	1618	TGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCA	1677
Qy	1412	TGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGC	1471
Db	1678	TAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGT	1737
Qy	1472	TGCTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCT	1531
Db	1738	GTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCT	1797
Qy	1532	CTCTGGTCA	1540

Db 1798 CCCTGCTGA 1806

RESULT 13

US-09-724-566A-44

; Sequence 44, Application US/09724566A  
; Patent No. 6627739  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, John P.  
; APPLICANT: Basi, Guribbal  
; APPLICANT: Doane, Minh Tam  
; APPLICANT: Frigon, No. 6627739mand  
; APPLICANT: John, Varghese  
; APPLICANT: Power, Michael  
; APPLICANT: Sinha, Sukanto  
; APPLICANT: Tatsuno, Gwen  
; APPLICANT: Tung, Jay  
; APPLICANT: Wang, Shuwen  
; APPLICANT: McConlogue, Lisa  
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and  
; TITLE OF INVENTION: Methods  
; FILE REFERENCE: 228-US-NEWC2  
; CURRENT APPLICATION NUMBER: US/09/724,566A  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/501,708  
; PRIOR FILING DATE: 2000-02-10  
; PRIOR APPLICATION NUMBER: 60/119,571  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 60/139,172  
; PRIOR FILING DATE: 1999-06-15  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 44  
; LENGTH: 2348  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-566A-44

Query Match 22.0%; Score 397.4; DB 4; Length 2348;  
Best Local Similarity 55.0%; Pred. No. 7.1e-85;  
Matches 863; Conservative 0; Mismatches 676; Indels 30; Gaps 3;

Qy 2 TGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCCG 61  
||||| ||| ||| ||| | ||| ||| ||||| || || | |  
Db 238 TGGGGGCAGGCGCCAGGGACGGACGTGGGCCAGTGCGAGCCCAGAGGGCCCGAAGGCCGG 297  
  
Qy 62 CCCCAGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAACC 121  
|| ||||| || | | ||| | || ||| ||||| | |  
Db 298 GGCCCACCATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGC 357  
  
Qy 122 GCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTGG 181  
| | | || | || | || || || | | |||  
Db 358 CTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCC 417  
  
Qy 182 CGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGC----- 224  
| || | ||| || ||| || | || || | |||

Db	418	CCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGG	477
Qy	225	-CAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGG	283
Db	478	GCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGG	537
Qy	284	AGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTA	343
Db	538	AGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTA	597
Qy	344	ACTTTGCCGTGGCAGGAACCCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT	403
Db	598	ACTTTGCAGTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGT	657
Qy	404	CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGA	463
Db	658	CCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGG	717
Qy	464	CGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTG	523
Db	718	AAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACGTGTGCGTG	777
Qy	524	TCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATG	583
Db	778	CCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAG	837
Qy	584	GAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCT	643
Db	838	GCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCT	897
Qy	644	TCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAG	703
Db	898	TTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTG	957
Qy	704	CCGGCTTGCCCGT-----TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGG	754
Db	958	CTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTG	1017
Qy	755	GTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGT	814
Db	1018	GAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGT	1077
Qy	815	GGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACT	874
Db	1078	GGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACT	1137
Qy	875	GCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGC	934
Db	1138	GCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGC	1197
Qy	935	CCCAGAAGGTGTTTGATGCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAAT	994
Db	1198	CCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGT	1257
Qy	995	TCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTT	1054
Db	1258	TCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTT	1317

Qy 1055 GGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCC 1114  
 || |||| |||| ||||| | | |||| || | ||| ||||  
 Db 1318 GGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCC 1377

Qy 1115 GTATCACAATCCTGCCTCAGCTTTACATTAGCCCATGATGGGGGCCGCCTG---AATT 1171  
 | |||| |||| | |||| || | | || | | | | | |  
 Db 1378 GCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAG 1437

Qy 1172 ATGAATGTTACCGATTTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGG 1231  
 | || |||| | | | || | | | | | | | || || || ||  
 Db 1438 ACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTA 1497

Qy 1232 TGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGA 1291  
 | ||||| ||||| |||| | |||| | | | |||| | | | |  
 Db 1498 TCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCA 1557

Qy 1292 GCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAG 1351  
 || | | | | | | | | | | | | | | || |||| | |  
 Db 1558 GCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCT 1617

Qy 1352 AGGATGTAGCCAGCAACTGTGTCCCGCTCAGTCTTTGAGCGAGCCATTTTGTGGATTG 1411  
 || | | | | | | | | | | | | | | || | | | |  
 Db 1618 TGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCA 1677

Qy 1412 TGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGC 1471  
 | |||| | | | |||| | | | || | | | | || || ||  
 Db 1678 TAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGT 1737

Qy 1472 TGCTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCT 1531  
 | | | | | | | | | | | | | | |||| | |  
 Db 1738 GTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCT 1797

Qy 1532 CTCTGGTCA 1540  
 | || | |  
 Db 1798 CCCTGCTGA 1806

# RESULT 14

US-09-724-566A-48

; Sequence 48, Application US/09724566A

; Patent No. 6627739

; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.

; APPLICANT: Basi, Gurigbal

; APPLICANT: Doane, Minh Tam

; APPLICANT: Frigon, No. 6627739mand

; APPLICANT: John, Varghese

; APPLICANT: Power, Michael

; APPLICANT: Sinha, Sukanto

; APPLICANT: Tatsuno, Gwen

; APPLICANT: Tung, Jay

; APPLICANT: Wang, Shuwen

; APPLICANT: McConlogue, Lisa

; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and

; TITLE OF INVENTION: Methods

; FILE REFERENCE: 228-US-NEWC2

```
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 16080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Expression Vector pCEK
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(16080)
; OTHER INFORMATION: n = A,T,C or G
US-09-724-566A-48
```

```
Query Match          22.0%;  Score 397.4;  DB 4;  Length 16080;
Best Local Similarity 55.0%;  Pred. No. 1.5e-84;
Matches 863;  Conservative 0;  Mismatches 676;  Indels 30;  Gaps 3;
```

```
Qy      2  TGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCCG 61
      |||| |||  ||| |||  |  ||| |||  ||||| ||  ||  |  |  |
Db      1607 TGGGGGCGAGGCGCCAGGGACGGACGTGGGCCAGTGCAGAGCCAGAGGGCCCGAAGGCCG 1666

Qy      62  CCCCAGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAACC 121
      ||  ||||| |||  |  |  ||| |  ||  || ||| |||||  |  |
Db      1667 GGCCCACCATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGC 1726

Qy     122  GCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTGG 181
      |  |  ||  |  ||  |  ||  ||  ||  ||  |  |  |  |||
Db     1727 CTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCC 1786

Qy     182  CGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGC----- 224
      | || |  ||| ||  ||| || | ||  ||  |  |||
Db     1787 CCCTGGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGG 1846

Qy     225  -CAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGG 283
      || ||| |||  ||||| ||||| |||  |  ||  ||  |  ||||| |||
Db     1847 GCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGG 1906

Qy     284  AGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTA 343
      |||||  | || |  ||||| ||||| |||  |  ||  ||  ||  ||  |||||
Db     1907 AGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTA 1966

Qy     344  ACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT 403
      ||||| ||||  |  |||| ||| |||  |  |  ||||  |  |  ||  ||
Db     1967 ACTTTGCAGTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGT 2026

Qy     404  CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGA 463
      |  ||||| |||||  |  |  |  ||  |||  ||||  ||  ||  |  |||
Db     2027 CCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGG 2086
```

Qy	464	CGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTG	523
Db	2087	AAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTG	2146
Qy	524	TCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATG	583
Db	2147	CCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAG	2206
Qy	584	GAATACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCT	643
Db	2207	GCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCT	2266
Qy	644	TCGACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAG	703
Db	2267	TTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTG	2326
Qy	704	CCGGCTTGCCCGT-----TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGG	754
Db	2327	CTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTG	2386
Qy	755	GTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGT	814
Db	2387	GAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGT	2446
Qy	815	GGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACT	874
Db	2447	GGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACT	2506
Qy	875	GCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGC	934
Db	2507	GCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGC	2566
Qy	935	CCCAGAAGGTGTTTGTATGCGGTGGTGGAAAGCTGTGGCCCGCGCATCTCTGATTCCAGAAT	994
Db	2567	CCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGT	2626
Qy	995	TCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTT	1054
Db	2627	TCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTT	2686
Qy	1055	GGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCC	1114
Db	2687	GGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCC	2746
Qy	1115	GTATCACAATCCTGCCTCAGCTTTACATTCAGCCCATGATGGGGGCCGGCCTG---AATT	1171
Db	2747	GCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAG	2806
Qy	1172	ATGAATGTTACCGATTTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGG	1231
Db	2807	ACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTA	2866
Qy	1232	TGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGA	1291
Db	2867	TCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCCGAAACGAATTGGCTTTGCTGTCA	2926

```

Qy      1292  GCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAG 1351
          || | ||   |   |   |   |   |   |   |   |   |   |
Db      2927  GCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCT 2986

Qy      1352  AGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTG 1411
          |||  | |   |   |   |   |   |   |   |   |   |
Db      2987  TGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCA 3046

Qy      1412  TGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGC 1471
          |  |||||  |   |   ||||  |   |   ||  |   |   ||  |
Db      3047  TAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGT 3106

Qy      1472  TGCTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCT 1531
          |  |  |  |  |   |   |  |  |  |  |  |  |  |  |  |  |
Db      3107  GTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCT 3166

Qy      1532  CTCTGGTCA 1540
          |  |||  |  |
Db      3167  CCCTGCTGA 3175

```

RESULT 15

US-09-724-566A-1

```

; Sequence 1, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurqbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-566A-1

```

Query Match

21.9%; Score 395; DB 4; Length 1503;



Best Local Similarity 55.6%; Pred. No. 2.2e-84;  
Matches 805; Conservative 0; Mismatches 630; Indels 12; Gaps 2;

```
Qy      106 GCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGC 165
      |||  | |||  | |||  | ||  ||  |||  | |  |||  | ||  ||
Db      55 GCCCACGGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCC 114

Qy      166 CACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCC 225
      |  |      | |||  | |  ||  | |  | |  | |  |||  |  |  |
Db      115 CTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC 174

Qy      226 AACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAG 285
      | |||  |||  |||||  |||||  |||  | ||  ||  | |||||  |||||
Db      175 AGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAG 234

Qy      286 ATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAAC 345
      |||  | ||  | |||||  |||  | ||  ||  ||  ||  ||  |||||
Db      235 ATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAAC 294

Qy      346 TTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTAATTTGACACAGAGAGGTCT 405
      |||||  ||||  |  ||||  |||  |||  | |  |  ||||  | |  ||  |||
Db      295 TTTGCAGTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCC 354

Qy      406 AGCACATAACGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG 465
      |||||  |||||  |  |  |  ||  ||  |||  |||||  ||  ||  | |||
Db      355 AGCACATAACGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAA 414

Qy      466 GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC 525
      ||  |  ||  |||||  ||  | |||||  | |||  |||  |  |  ||  |
Db      415 GGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACCTGTGCGTGCC 474

Qy      526 AACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGA 585
      |||||  ||  ||  |||||  ||  |||||  |  ||  ||  ||  ||  ||
Db      475 AACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGC 534

Qy      586 AACTTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTC 645
      ||  ||  ||  ||  ||  |||||  |||||  |||  ||  |||||  | |||||
Db      535 ATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTT 594

Qy      646 GACTCCCTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCC 705
      |||||  |||||  |  ||  |  ||  | |||||  | |||||  |||||  ||
Db      595 GACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCT 654

Qy      706 GGCTTGCCCGT-----TGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGT 756
      |||||  |||  |  ||  |  |  |  |||||  ||  |  ||  ||
Db      655 GGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGA 714

Qy      757 GGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGG 816
      ||  ||  ||  |  |||  | |||  |||||  ||  ||  |  |||||
Db      715 GGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACCCCATCCGGCGGGAGTGG 774

Qy      817 TACTACCAGATAGAAATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGC 876
      ||  ||  ||  |  |||  ||  ||||  ||  ||  ||  ||  |||||
Db      775 TATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGC 834

Qy      877 AGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCC 936
      |  |||||  |||  |||||  |||  |||||  |||||  ||  ||  |||||
```

Db 835 AAGGAGTACAACCTATGACAAGAGCATTTGTGGACAGTGGCACCACCAACCTTCGTTTGCCC 894  
 Qy 937 CAGAAGGTGTTTGATGCGGTGGTGAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTC 996  
 |||| ||||| || | || || | | || || | |||  
 Db 895 AAGAAAGTGTGTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTC 954  
 Qy 997 TCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGG 1056  
 ||||| ||||| || ||||| ||||| || |||||  
 Db 955 CCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGG 1014  
 Qy 1057 TCTTACTTCCCTAAAATCTCCATCTACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGT 1116  
 ||||| ||||| ||||| | | |||| ||| | ||| |||||  
 Db 1015 AACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGC 1074  
 Qy 1117 ATCACAATCCTGCCTCAGCTTTACATTCAGCCCATG---ATGGGGGCCGGCCTGAATTAT 1173  
 ||||| ||||| || |||| ||| | | ||| || | |||| | |  
 Db 1075 ATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGAC 1134  
 Qy 1174 GAATGTTACCGATTTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACGGTG 1233  
 || ||||| || | ||| || | || | | || || || || |  
 Db 1135 GACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATC 1194  
 Qy 1234 ATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGC 1293  
 ||||| ||||| |||| || | |||| || | | |||| || | |||  
 Db 1195 ATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGC 1254  
 Qy 1294 CCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAG 1353  
 | || | | | | | | | | || |||| | | |  
 Db 1255 GCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTG 1314  
 Qy 1354 GATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTG 1413  
 || | | | | | | || || | | || | | || |  
 Db 1315 GACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATA 1374  
 Qy 1414 TCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTG 1473  
 ||||| | | |||| | || | || | | || | || ||  
 Db 1375 GCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGT 1434  
 Qy 1474 CTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTCGTCAATGATGAGTCCTCT 1533  
 | | | | | | | | || | | || | | ||||| |||  
 Db 1435 CAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCC 1494  
 Qy 1534 CTGGTCA 1540  
 ||| ||  
 Db 1495 CTGCTGA 1501

Search completed: February 28, 2004, 07:06:31  
 Job time : 163 secs

OM nucleic - nucleic search, using sw model

Run on: February 28, 2004, 05:52:24 ; Search time 637 Seconds  
(without alignments)  
10216.436 Million cell updates/sec

Title: US-09-668-314C-1  
Perfect score: 1804  
Sequence: 1 atgggcgcactggcccgggc.....aaaccaaaaaaaaaaaaaaa 1804

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2353733 seqs, 1803733377 residues

Total number of hits satisfying chosen parameters: 4707466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
					Description

1	1804	100.0	1804	9	US-09-794-927-1	Sequence 1, Appli
2	1804	100.0	1804	9	US-09-795-847-1	Sequence 1, Appli
3	1804	100.0	1804	9	US-09-794-743-1	Sequence 1, Appli
4	1804	100.0	1804	9	US-09-794-748-1	Sequence 1, Appli
5	1804	100.0	1804	9	US-09-794-925-1	Sequence 1, Appli
6	1804	100.0	1804	9	US-09-681-442-1	Sequence 1, Appli
7	1804	100.0	1804	10	US-09-869-414-1	Sequence 1, Appli
8	1804	100.0	1804	10	US-09-548-366-1	Sequence 1, Appli
9	1784.4	98.9	1879	9	US-09-978-295A-195	Sequence 195, App
10	1784.4	98.9	1879	9	US-09-978-697-195	Sequence 195, App
11	1784.4	98.9	1879	9	US-09-978-192A-195	Sequence 195, App
12	1784.4	98.9	1879	9	US-09-999-832A-195	Sequence 195, App
13	1784.4	98.9	1879	10	US-09-978-189-195	Sequence 195, App
14	1784.4	98.9	1879	10	US-09-978-608A-195	Sequence 195, App
15	1784.4	98.9	1879	10	US-09-978-585A-195	Sequence 195, App
16	1784.4	98.9	1879	10	US-09-978-191A-195	Sequence 195, App
17	1784.4	98.9	1879	10	US-09-978-403A-195	Sequence 195, App
18	1784.4	98.9	1879	10	US-09-978-564A-195	Sequence 195, App
19	1784.4	98.9	1879	10	US-09-999-833A-195	Sequence 195, App
20	1784.4	98.9	1879	10	US-09-981-915A-195	Sequence 195, App
21	1784.4	98.9	1879	10	US-09-978-824-195	Sequence 195, App
22	1784.4	98.9	1879	10	US-09-918-585A-195	Sequence 195, App
23	1784.4	98.9	1879	10	US-09-978-423A-195	Sequence 195, App
24	1784.4	98.9	1879	10	US-09-978-193A-195	Sequence 195, App
25	1784.4	98.9	1879	10	US-09-999-830A-195	Sequence 195, App
26	1784.4	98.9	1879	10	US-09-978-757A-195	Sequence 195, App
27	1784.4	98.9	1879	10	US-09-978-187B-195	Sequence 195, App
28	1784.4	98.9	1879	10	US-09-978-643A-195	Sequence 195, App
29	1784.4	98.9	1879	10	US-09-978-375A-195	Sequence 195, App
30	1784.4	98.9	1879	10	US-09-978-298A-195	Sequence 195, App
31	1784.4	98.9	1879	10	US-09-978-188A-195	Sequence 195, App
32	1784.4	98.9	1879	10	US-09-978-681A-195	Sequence 195, App
33	1784.4	98.9	1879	10	US-09-978-194A-195	Sequence 195, App
34	1784.4	98.9	1879	10	US-09-999-829A-195	Sequence 195, App
35	1784.4	98.9	1879	10	US-09-978-299A-195	Sequence 195, App
36	1784.4	98.9	1879	10	US-09-978-544A-195	Sequence 195, App
37	1784.4	98.9	1879	10	US-09-978-665A-195	Sequence 195, App
38	1784.4	98.9	1879	10	US-09-978-802A-195	Sequence 195, App
39	1784.4	98.9	1879	12	US-10-164-749A-195	Sequence 195, App
40	1784.4	98.9	1879	12	US-10-206-915-71	Sequence 71, Appl
41	1784.4	98.9	1879	12	US-10-199-670-71	Sequence 71, Appl
42	1784.4	98.9	1879	13	US-10-052-586-71	Sequence 71, Appl
43	1784.4	98.9	1879	14	US-10-174-590-71	Sequence 71, Appl
44	1784.4	98.9	1879	14	US-10-176-758-71	Sequence 71, Appl
45	1784.4	98.9	1879	14	US-10-175-737-71	Sequence 71, Appl

#### ALIGNMENTS

RESULT 1  
 US-09-794-927-1  
 ; Sequence 1, Application US/09794927  
 ; Patent No. US20010016324A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gurney, Mark E.

```

; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-927-1

```

```

Query Match          100.0%; Score 1804; DB 9; Length 1804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy    121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

```

Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260

```

Db      1201 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC 1260
Qy      1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
      |||
Db      1261 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA 1320
Qy      1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
      |||
Db      1321 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT 1380
Qy      1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
      |||
Db      1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440
Qy      1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
      |||
Db      1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC 1500
Qy      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
      |||
Db      1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560
Qy      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
      |||
Db      1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620
Qy      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1680
      |||
Db      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1680
Qy      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
      |||
Db      1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740
Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
      |||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA 1800
Qy      1801 AAAA 1804
      |||
Db      1801 AAAA 1804

```

## RESULT 2

US-09-795-847-1

; Sequence 1, Application US/09795847

; Patent No. US20010018208A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND

; TITLE OF INVENTION: USES



; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 28341/6280DE  
; CURRENT APPLICATION NUMBER: US/09/795,847  
; CURRENT FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 09/416,901  
; PRIOR FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1804  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-795-847-1

Query Match 100.0%; Score 1804; DB 9; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACCTTCTTGGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACCTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480

Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320

Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAAAACTTCATTCTAAACCAAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

### RESULT 3

US-09-794-743-1

; Sequence 1, Application US/09794743

; Patent No. US20010021391A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280BC

; CURRENT APPLICATION NUMBER: US/09/794,743

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1804  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-794-743-1

Query Match 100.0%; Score 1804; DB 9; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy    121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC 420

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540

Qy    541 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440

Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCAGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

#### RESULT 4

US-09-794-748-1

; Sequence 1, Application US/09794748

; Patent No. US20020037315A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280JL

; CURRENT APPLICATION NUMBER: US/09/794,748

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1804  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-794-748-1

Query Match 100.0%; Score 1804; DB 9; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720



Db	661	 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	 CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	 TACCTGAGAGATGAGAACTCCAGCAGGTCAATCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCTGCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560

Db 1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560  
 Qy 1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620  
 Qy 1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680  
 Qy 1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740  
 Qy 1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA 1800  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA 1800  
 Qy 1801 AAAA 1804  
 ||||  
 Db 1801 AAAA 1804

RESULT 5

US-09-794-925-1

; Sequence 1, Application US/09794925

; Patent No. US20020064819A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280HI

; CURRENT APPLICATION NUMBER: US/09/794,925

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 1804

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-794-925-1

Query Match 100.0%; Score 1804; DB 9; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Qy	61	GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC AACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840

Db	781	 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTGCTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	 CGTGACCCTGAGGTGCTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680

```

Db      1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680

Qy      1681 GCTCCCAGATGCCTTCTAGATTCACCTGTCTTTTGATTCTTGATTTTCAAGCTTCAAATC 1740
          |||
Db      1681 GCTCCCAGATGCCTTCTAGATTCACCTGTCTTTTGATTCTTGATTTTCAAGCTTCAAATC 1740

Qy      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA 1800
          |||
Db      1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA 1800

Qy      1801 AAAA 1804
          |||
Db      1801 AAAA 1804

```

RESULT 6

US-09-681-442-1

; Sequence 1, Application US/09681442

; Patent No. US20020081634A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280FG

; CURRENT APPLICATION NUMBER: US/09/681,442

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 1804

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-681-442-1

Query Match 100.0%; Score 1804; DB 9; Length 1804;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
          |||
Db      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

```

Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960



Db	901	 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Db	1141	 ATTCAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1441	 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800



Db 1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAAAAA 1800

Qy 1801 AAAA 1804  
||||

Db 1801 AAAA 1804

RESULT 7

US-09-869-414-1

; Sequence 1, Application US/09869414

; Publication No. US20030077226A1

; GENERAL INFORMATION:

; APPLICANT: Beinkowski et al.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280M

; CURRENT APPLICATION NUMBER: US/09/869,414

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 1804

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-869-414-1

Query Match 100.0%; Score 1804; DB 10; Length 1804;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60  
|||||

Db 1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60

Qy 61 GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120  
|||||

Db 61 GCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120

Qy 121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180  
|||||

Db 121 CGCGTAGTTGCGECCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180

Qy 181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240  
|||||

Db 181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240

Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Qy	301	CCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Db	301	CCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGA	360
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140

Db	1081	 TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Db	1141	 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Db	1321	 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	 GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

RESULT 8

US-09-548-366-1

; Sequence 1, Application US/09548366

; Publication No. US20030104365A1

; GENERAL INFORMATION:

```

; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 28341/6280A
; CURRENT APPLICATION NUMBER: US/09/548,366
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-366-1

```

Db	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260

Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Db	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAAACCAAAAAAAAAA	1800
Qy	1801	AAAA 1804	
Db	1801	AAAA 1804	

# RESULT 9

US-09-978-295A-195

; Sequence 195, Application US/09978295A

; Patent No. US20020156006A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664



; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079786  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080328  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080334  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/081070  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081049  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081071  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081195  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082569  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082704  
; PRIOR FILING DATE: 1998-04-22

; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082700  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082797  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083392  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083495  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083496  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083499  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083554  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083558  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083742  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 60/084366  
; PRIOR FILING DATE: 1998-05-05  
; PRIOR APPLICATION NUMBER: 60/084414  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323

; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.9%; Score 1784.4; DB 9; Length 1879;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	94	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	153
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	154	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	213
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	214	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	273
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	274	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	334	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	393
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	394	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	453
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633

Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCTCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCTCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440

Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCACGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1879

RESULT 10

US-09-978-697-195

; Sequence 195, Application US/09978697

; Patent No. US20020169284A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James;  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C27  
; CURRENT APPLICATION NUMBER: US/09/978,697  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079786  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105

; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080328  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080334  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/081070  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081049  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081071  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081195  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082569  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082704  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082700  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082797  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083392  
; PRIOR FILING DATE: 1998-04-29



; PRIOR APPLICATION NUMBER: 60/083495  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083496  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083499  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083554  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083558  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083742  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 60/084366  
; PRIOR FILING DATE: 1998-05-05  
; PRIOR APPLICATION NUMBER: 60/084414  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-5-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704

; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.9%; Score 1784.4; DB 9; Length 1879;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     94 ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy    121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy    181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333

Qy    241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy    301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy    361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC 513

Qy    421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

Qy    481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633

Qy    541 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT 693

Qy    601 TATGCCCACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 TATGCCCACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA 753

Qy    661 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT 813

Qy    721 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713

Qy 1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1680  
 |||  
 Db 1714 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT 1773  
 Qy 1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740  
 |||  
 Db 1774 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1833  
 Qy 1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA 1786  
 |||  
 Db 1834 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA 1879

RESULT 11

US-09-978-192A-195

; Sequence 195, Application US/09978192A

; Patent No. US20020177553A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James;  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C9

; CURRENT APPLICATION NUMBER: US/09/978,192A

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079786  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080328  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080334

; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/081070  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081049  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081071  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081195  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082569  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082704  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082700  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082797  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083392  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083495  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083496  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083499  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083554  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083558  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29

```

; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

```

```

Query Match          98.9%;  Score 1784.4;  DB 9;  Length 1879;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 1785;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

```

```

Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy     61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213

```



Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	214	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	273
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	274	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	334	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	393
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	394	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	453
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053

Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1879

RESULT 12

US-09-999-832A-195

; Sequence 195, Application US/09999832A

; Publication No. US20020192706A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C63

; CURRENT APPLICATION NUMBER: US/09/999,832A

; CURRENT FILING DATE: 2001-10-24

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077791

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079786  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080328  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080334  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/081070  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081049  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081071  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081195  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081955

; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082569  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082704  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082700  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082797  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083392  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083495  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083496  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083499  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083554  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083558  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083742  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 60/084366  
; PRIOR FILING DATE: 1998-05-05  
; PRIOR APPLICATION NUMBER: 60/084414  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07

```
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
```

```
Query Match          98.9%;  Score 1784.4;  DB 9;  Length 1879;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 1785;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;
```

```
Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy     121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333

Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
```

Db	394	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	453
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATCTGAAA	840
Db	874	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCA	1200



Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440
Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCAGTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1879

# RESULT 13

US-09-978-189-195

; Sequence 195, Application US/09978189

; Publication No. US20030004102A1

## ; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C7  
; CURRENT APPLICATION NUMBER: US/09/978,189  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079664  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079786  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080328  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080334  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/081070  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081049  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081071  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081195  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082569  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082704

; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082700  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082797  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083392  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083495  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083496  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083499  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083554  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083558  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083742  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 60/084366  
; PRIOR FILING DATE: 1998-05-05  
; PRIOR APPLICATION NUMBER: 60/084414  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-5-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13

; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.9%; Score 1784.4; DB 10; Length 1879;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	94	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	153
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	154	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	213
Qy	121	CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	214	CGCGTAGTTGCGCCCAACCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	273
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	274	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	334	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	393
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	394	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	453
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	420
Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633

Qy	541	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473

Qy 1381 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1440  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1474 CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA 1533  
 Qy 1441 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC 1500  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1534 GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC 1593  
 Qy 1501 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1560  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1594 CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA 1653  
 Qy 1561 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1620  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1654 GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC 1713  
 Qy 1621 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1680  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1714 AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT 1773  
 Qy 1681 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1740  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1774 GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC 1833  
 Qy 1741 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA 1786  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1834 CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA 1879

RESULT 14

US-09-978-608A-195

; Sequence 195, Application US/09978608A

; Publication No. US20030045462A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James;  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.



```

; APPLICANT:  Stewart, Timothy A.
; APPLICANT:  Tumas, Daniel
; APPLICANT:  Williams, P. Mickey
; APPLICANT:  Wood, William I.
; TITLE OF INVENTION:  Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION:  Acids Encoding the Same
; FILE REFERENCE:  P2630PlC22
; CURRENT APPLICATION NUMBER:  US/09/978,608A
; CURRENT FILING DATE:  2001-10-16
; NUMBER OF SEQ ID NOS:  624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 195
;   LENGTH: 1879
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-978-608A-195

```

```

Query Match          98.9%;  Score 1784.4;  DB 10;  Length 1879;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 1785;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

```

```

Qy      1 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      94 ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC 153

Qy      61 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC 213

Qy     121 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 180
        ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     214 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG 273

Qy     181 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     274 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG 333

Qy     241 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC 393

Qy     301 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA 453

Qy     361 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     454 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATAACCGCTCC 513

Qy     421 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA 573

Qy     481 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     574 GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT 633

```

Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600
Db	634	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	GGAGACATCTGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	CAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1200
Db	1234	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440

Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACCTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCACCTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1879

RESULT 15

US-09-978-585A-195

; Sequence 195, Application US/09978585A

; Publication No. US20030049633A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C15  
; CURRENT APPLICATION NUMBER: US/09/978,585A  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 195  
; LENGTH: 1879  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-978-585A-195

Query Match 98.9%; Score 1784.4; DB 10; Length 1879;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	60
Db	94	ATGGGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCCAGTGGCTCCTGCGCGCC	153
Qy	61	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	120
Db	154	GCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC	213
Qy	121	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	180
Db	214	CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG	273
Qy	181	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	240
Db	274	GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCCGCCAACTTCTTGGCCATG	333
Qy	241	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	300
Db	334	GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC	393
Qy	301	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	360
Db	394	CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTTGCCGTGGCAGGA	453
Qy	361	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	420
Db	454	ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC	513
Qy	421	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	480
Db	514	AAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA	573
Qy	481	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	540
Db	574	GACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACTATT	633
Qy	541	TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	600

Db	634	 TTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT	693
Qy	601	TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	660
Db	694	 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA	753
Qy	661	CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	720
Db	754	 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCT	813
Qy	721	GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	780
Db	814	 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA	873
Qy	781	GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	840
Db	874	 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAA	933
Qy	841	TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	900
Db	934	 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC	993
Qy	901	ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	960
Db	994	 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG	1053
Qy	961	GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1020
Db	1054	 GAAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC	1113
Qy	1021	CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1080
Db	1114	 CAGCTGGCGTGCTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC	1173
Qy	1081	TACCTGAGAGATGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1140
Db	1174	 TACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTAC	1233
Qy	1141	ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1200
Db	1234	 ATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCA	1293
Qy	1201	TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1260
Db	1294	 TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC	1353
Qy	1261	AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1320
Db	1354	 AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCA	1413
Qy	1321	GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1380
Db	1414	 GTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT	1473
Qy	1381	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1440

Db	1474	CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGA	1533
Qy	1441	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGTCAGCGTCGCCCC	1500
Db	1534	GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGTCAGCGTCGCCCC	1593
Qy	1501	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1560
Db	1594	CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA	1653
Qy	1561	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1620
Db	1654	GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC	1713
Qy	1621	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1680
Db	1714	AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT	1773
Qy	1681	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1740
Db	1774	GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC	1833
Qy	1741	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1786
Db	1834	CTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA	1879

Search completed: February 28, 2004, 08:48:42  
 Job time : 645 secs